59946

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	TYPE OF SEARCH:	VENDOR/COST(where applic.)
Searcher:	NA Sequences:	STN:
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Online time:	Other:	Other (specify):

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     FILE 'USPATFULL' ENTERED AT 14:31:57 ON 09 FEB 2002
                  E MARCHALONIS J J/IN
L1              2 S E4
                  E WATSON RONALD R/IN
L2              3 S E3
                  E SCHLUTER SAMUEL F/IN
L3           3644 S (T-CELL RECEPTOR OR TCR)
L4           2225 S L3 AND (PEPTIDE? OR POLYPEPTIDE?)
L5              0 S L4 AND (CKPISGHNSLFWYRQT)
L6            241 S L4 AND (TH1 OR TH2 OR TH0)
L7            139 S L6 AND (HIV OR SIV OR FIV OR EIAV OR BIV OR CAEV)
L8             12 S L7 AND (TH1/CLM OR TH2/CLM OR TH0/CLM)
L9            289 S (TCR/CLM OR T-CELL RECEPTOR/CLM)
L10           185 S L9 AND L4
L11            94 S L10 AND (PEPTIDE/CLM OR POLYPEPTIDE/CLM)

     FILE 'MEDLINE' ENTERED AT 14:44:05 ON 09 FEB 2002
                  E MARCHALONIS J J/AU
L12           237 S E3-E4
L13             3 S L12 AND (TH1 OR TH2 OR TH0)
L14             4 S L12 AND (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L15             4 S L14 NOT L13
L16           230 S L12 NOT (L13 OR L14)
                  E WATSON R R/AU
L17           246 S E3
L18           242 S L17 NOT L16
L19            17 S L18 AND (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L20            10 S L18 AND (TH1 OR TH2 OR TH0)
L21            10 S L20 NOT L19
                  E SCHLUTER S F/AU
L22            78 S E3
L23            10 S L22 NOT (L12 OR L17)

     FILE 'WPIDS' ENTERED AT 15:01:07 ON 09 FEB 2002
                  E MARCHALONIS J J/IN
L24             3 S E3

     FILE 'MEDLINE' ENTERED AT 15:03:40 ON 09 FEB 2002
L25        113498 S (HIV OR HUMAN IMMUNODEFICIENCY VIRUS)
L26           461 S L25 AND (TH1 OR TH2 OR TH0)
L27           185 S L26 AND (MODULATION OR TREATMENT OR THERAP? OR REGULATION)
                  E FAUCI A/AU
L28           729 S E4
L29             2 S L28 AND (TH1 OR TH2 OR TH0)
L30            16 S L28 AND (IMMUNOPATHOGENESIS OR CYTOKINE DYSREGULATION)
L31            62 S L28 AND (IL-2 OR IL-4 OR IL-10)
L32             0 S L31 AND (TCR OR T-CELL RECEPTOR)
L33            11 S L28 AND (TCR OR T-CELL RECEPTOR)
L34            33 S L26 AND (THO OR TH0)
L35           626 S L25 AND (CYTOKINE THERAPY OR IMMUNOTHERAPY)
L36            77 S L35 AND (IL-2 OR INTERLEUKIN-2)
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L1 ANSWER 1 OF 2 USPATFULL
1999:67011 T-cell receptor peptides and methods for preventing the progression to AIDS in an animal model.
Marchalonis, John J. , Tucson, AZ, United States
Watson, Ronald R., Tucson, AZ, United States
Dehghanpisheh, Keivan, Portland, OR, United States
Wang, Yuejian, St. Paul, MN, United States
Huang, Dennis S., Shaker Heights, OH, United States
Arizona Board of Regents on Behalf of the University of Arizona, Tucson, AZ, United States (U.S. corporation)
US 5911990 19990615
APPLICATION: US 1996-696049 19960813 (8)
DOCUMENT TYPE: Utility; Granted.
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

AB A novel peptide from the T-cell receptor is shown to be effective in preventing the progression to AIDS in an animal model. Methods for delaying the progression to AIDS and restoring normal immunological responses in an animal model following infection are shown and comprise administering through various systemic routes T-cell receptor peptide V.beta. CDR1 to restore normal levels of Th1 cytokines interleukin 2 and interferon-.gamma., which are suppressed following infection, and those of Th2 derived cytokines interleukin 5, interleukin 6, interleukin 10, and immunoglobulin G, which are stimulated following infection.

CLM What is claimed is:

1. A method of modulating the immune response in a mammal infected with a C-type retrovirus or a lentivirus, comprising administering by a systemic route an amount of T-cell receptor V.beta. CDR1 peptide of SEQ ID NO:1 sufficient to stimulate the production of interleukin 2 and interferon-.gamma., and to suppress the production of interleukin 5, interleukin 6, interleukin 10, and immunoglobulin G.

2. The method of claim 1, wherein said lentivirus comprises HIV.

3. A method of altering the immune system response of a host infected with a C-type retrovirus or a lentivirus, comprising artificially introducing a T-cell receptor V.beta. CDR1 peptide of SEQ ID NO: 1 into the bloodstream or immune system by injection so as to artificially induce said immune system to stimulate production of Th1 cytokines or suppress production of Th2 derived cytokines.

4. The method of claim 3, wherein said lentivirus comprises HIV.

5. The method of claim 3, wherein said lentivirus comprises feline immunodeficiency virus.

6. A method of altering the immune system response of a host suffering from an infectious disease comprising artificially introducing a T-cell receptor V.beta. CDR1 peptide of SEQ ID NO: 1 into the bloodstream or immune system by injection so as to artificially induce said immune system to stimulate production of Th1 cytokines or suppress production of Th2 derived cytokines.

L15 ANSWER 1 OF 4 MEDLINE
1999326382 Document Number: 99326382. PubMed ID: 10398407. Recognition of defined epitopes by affinity-purified anti-immunoglobulin fab autoantibodies isolated from ***HIV*** -infected humans.
Marchalonis J J ; Garza A; Lake D F; Landsperger W J; Susal C. (Microbiology and Immunology, College of Medicine, Arizona Health Sciences Center, P.O. Box 24-5049, Tucson AZ 85724, USA.. dianah@u.arizona.edu) . JOURNAL OF MOLECULAR RECOGNITION, (1999 May-Jun) 12 (3) 169-76. Journal code: AOO; 9004580. ISSN: 0952-3499. Pub. country: ENGLAND: United Kingdom. Language: English.

AB Infection of humans with ***HIV*** -1 has previously been independently shown to result in the generation of autoantibodies (AAbs) reactive with immunoglobulin Fab fragments (Heidelberg), and with autoantibodies to T-cell receptors (TCRs) (Tucson). Here, we carry out epitope mapping studies of affinity-purified AAbs to Fab fragments prepared from individual ***HIV*** -positive patients for their capacity to bind recombinant constructs and peptide-defined epitopes modeling TCR and Ig light chains. Some affinity-purified autoantibodies reacted strongly with TCRs expressed by intact T-cells, and recombinant Valpha/Vbeta constructs as well as with certain synthetic peptide epitopes. The binding reactions of affinity-purified AAbs of individual patients were distinct, and the AAb preparations consisted of populations of polyclonal lgs as reflected in specificity and isotype. AAb pools from individual patients all bound particular regions of TCR and Ig chains defined by comprehensive peptide synthesis including the CDR1 and Fr3 segments of the variable domains and the joining segment/switch peptide. In addition, other reactivities to restricted regions of alpha, beta and lambda light chains were documented. These results substantiate the cross-reactivity of TCR and Ig-Fab determinants, and are consistent with the hypothesis that autoantibodies arising as a consequence of ***HIV*** infection can have an immunomodulatory role.

L15 ANSWER 2 OF 4 MEDLINE
97153482 Document Number: 97153482. PubMed ID: 9000486. Analysis of autoantibodies to T-cell receptors among ***HIV*** -infected individuals: epitope analysis and time course. ***Marchalonis J J*** ; Ampel N M; Schluter S F; Garza A; Lake D F; Galgiani J N; Landsperger W J. (College of Medicine, University of Arizona, Tucson, Arizona, 85724, USA.) CLINICAL IMMUNOLOGY AND IMMUNOPATHOLOGY, (1997 Feb) 82 (2) 174-89. Journal code: DEA; 0356637. ISSN: 0090-1229. Pub. country: United States. Language: English.

AB Individuals seropositive for ***human*** ***immunodeficiency*** ***virus*** type 1 (***HIV***) express elevated levels of autoantibodies (AAbs) directed against recombinant T-cell receptors (TCRs) and synthetic peptide epitopes duplicating beta chain markers. We performed longitudinal studies of anti-TCR AAbs in ***HIV*** -1-infected individuals, making comparisons with uninfected sera and sera from other individuals infected with a nonviral agent. We determined levels of autoantibodies by titration using enzyme-linked immunosorbent assay (ELISA) and developed a means for characterizing "autoantibody CDR recognition spectrotypes" for individual sera. Antibody levels against certain defined synthetic epitopes were substantially elevated in ***HIV*** -infected subjects relative to reactivities by control groups. Individual sera showed relatively high AAb levels to a subset of CDR1 peptide epitopes. Two patients who subsequently developed AIDS showed particular reactivity to Vbeta2.1, 8.1, 10.1, and 22.1 epitopes. Our results show that production AAbs to TCR Vbeta epitopes is a general

consequence of ***HIV*** infection. The response is individual but shows some restriction and shifts in AAb subpopulations often occur with time.

L15 ANSWER 3 OF 4 MEDLINE
96229155 Document Number: 96229155. PubMed ID: 8644504. Autoantibodies against peptide-defined epitopes of T-cell receptors in retrovirally infected humans and mice. ***Marchalonis J J*** ; Lake D F; Schluter S F; Dehghanpisheh K; Watson R R; Ampel N M; Galgiani J N. (University of Arizona, Tucson, USA.) ADVANCES IN EXPERIMENTAL MEDICINE AND BIOLOGY, (1995) 383 211-22. Journal code: 2LU; 0121103. ISSN: 0065-2598. Pub. country: United States. Language: English.

AB Autoantibodies directed against peptide-defined epitopes of T-cell receptors occur in the serum of healthy humans with the levels and isotypic expression dependent upon physiological changes (aging, pregnancy) or upon the development of autoimmune disease. We carried out investigations of autoantibodies against Tcr peptide-defined epitopes in retroviral infections of humans (***HIV*** -1) and mice (LP-BM5 strain of murine leukemia virus) to determine whether infection with these agents disrupted the regulation of the production of these antibodies. Retroviral infection in humans resulted in increased levels of autoantibody production against putative immunoregulatory regions of the Tcr beta chain (V beta CDR1 and Fr3), a result reflecting a disruption of regulation. In addition, antigenic mimicry was observed with a cross-reaction shared between the common portion of the V3 neutralizing loop of the ***HIV*** -1 gp120 molecule and the joining segment of T-cell receptors (J beta). Infection of mice with the defective retrovirus resulted in the induction of antibodies directed particularly against V beta CDR1 peptide-defined determinants. Analysis of the virally induced response to a set of 8 CDR1 peptide epitopes indicated a selectivity to the process. It was possible to partially reverse aberrant cytokine changes correlated with the onset of murine MAIDS by administration of T-cell receptor peptides in saline. These results show that retroviral infection in humans and mice has a profound dysfunctional effect on the regulation of autoantibodies to T-cell receptors. The function of these autoantibodies in the immunopathogenesis of acquired immunodeficiency remains to be determined.

L15 ANSWER 4 OF 4 MEDLINE
95062162 Document Number: 95062162. PubMed ID: 7971973. Autoantibodies to the alpha/beta T-cell receptors in ***human*** ***immunodeficiency*** ***virus*** infection: dysregulation and mimicry. Lake D F; Schluter S F; Wang E; Bernstein R M; Edmundson A B; ***Marchalonis J J*** . (College of Medicine, University of Arizona, Tucson 85724.) PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1994 Nov 8) 91 (23) 10849-53. Journal code: PV3; 7505876. ISSN: 0027-8424. Pub. country: United States. Language: English.

AB Autoimmune reactivity is a consequence of infection with ***human*** ***immunodeficiency*** ***virus*** (***HIV***). We studied serological cross-reactions of purified pooled IgG from sera of ***HIV*** -infected individuals by using nested sets of synthetic overlapping peptides duplicating the covalent structures of T-cell receptors (TCRs) and immunoglobulin light chains and report that two processes of autoantibody production occur. (i) IgG autoantibodies to putative regulatory variable domain CDR1 and FR3 epitopes (where CDR is complementarity-determining region and FR is framework region) are present in pooled IgG from ***HIV*** -infected individuals at levels 10-fold greater than that in pooled IgG from healthy humans. (ii) Anti-TCR autoimmunization involves antigenic mimicry between a conserved peptide

stretch of the major neutralizing V3 loop determinant of ***HIV*** -1 gp120 and the conserved FR4 segment of the TCR V beta. Affinity-purified antibodies to the synthetic V3 loop peptide bound to a recombinant single-chain TCR and to a synthetic TCR joining segment peptide containing the FR4 sequence. Conversely, affinity-purified autoantibodies from pooled IgG from ***HIV*** -infected individuals to the TCR peptide bound the V3 loop peptide and a single-chain TCR. Inhibition studies indicated that the cross-reactive immunizing antigen was the V3 loop. These results bear upon the impact of ***HIV*** infection on immune regulation and on the selection of peptides for vaccine development.

L21 ANSWER 9 OF 10 MEDLINE
95363196 Document Number: 95363196. PubMed ID: 7636274. T cell receptor V beta complementarity-determining region 1 peptide administration moderates immune dysfunction and cytokine dysregulation induced by murine retrovirus infection. ***Watson R R*** ; Wang J Y; Dehghanpisheh K; Huang D S; Wood S; Ardestani S K; Liang B; Marchalonis J J. (Department of Family and Community Medicine, University of Arizona College of Medicine, Tucson 85724, USA.) JOURNAL OF IMMUNOLOGY, (1995 Aug 15) 155 (4) 2282-91. Journal code: IFB; 2985117R. ISSN: 0022-1767. Pub. country: United States. Language: English.

AB Murine AIDS, induced by LP-BM5 murine leukemia retrovirus infection, causes a progressive and profound immunodeficiency in female C57B1/6 mice. Previously, we reported that autoantibodies were elevated during the initiation phases of this murine retrovirus infection and bound peptide determinants corresponding to CDR1 of several TCR V beta-chains. Therefore, we designed studies to determine whether administration of a major autoimmunogenic TCR V beta CDR1 peptide before or after infection with LP-BM5 retrovirus would modulate retrovirus-induced dysregulation of T cell function. Administration of the TCR V beta CDR1 peptide before murine retrovirus infection significantly prevented its suppression of splenic NK cell activity, T and B cell proliferation, and monokine (IL-6 and TNF-alpha) and ***Th1*** cytokine (IL-2 and IFN-gamma) release by splenocytes, and inhibited retrovirus-induced elevation of ***Th2*** cytokine (IL-5 and IL-10). Similar data were obtained with peptide immunization 2 wk after murine retrovirus infection at 6 and 16 wk postinfection. However, delaying peptide immunization until severe suppression of T and B cell mitogenesis had occurred did not restore their functions. Immunization with TCR V beta peptide prevents development of retrovirus-induced immune dysfunction, which suggests a possible pathogenic role of autoreactive T cells as regulatory elements.

L27 ANSWER 184 OF 185 MEDLINE
93039657 Document Number: 93039657. PubMed ID: 1418612. T helper cell immune dysfunction in asymptomatic, ***HIV*** -1-seropositive individuals: the role of ***TH1*** - ***TH2*** cross- ***regulation*** . Shearer G M; Clerici M. (Experimental Immunology Branch, National Cancer Institute, National Institutes of Health, Bethesda, Md.) CHEMICAL IMMUNOLOGY, (1992) 54 21-43. Ref: 116. Journal code: AF7; 9001090. ISSN: 1015-0145. Pub. country: Switzerland. Language: English.

L27 ANSWER 176 OF 185 MEDLINE
95151146 Document Number: 95151146. PubMed ID: 7848519. The ***Th1*** - ***Th2*** hypothesis of ***HIV*** infection: new insights. Clerici M; Shearer G M. (Cattedra di Immunologia, Universita degli Studi, Milano, Italy.) IMMUNOLOGY TODAY, (1994 Dec) 15 (12) 575-81. Ref: 104. Journal code: AEA; 8008346. ISSN: 0167-5699. Pub. country: ENGLAND: United Kingdom. Language: English.

AB In their earlier, much quoted, viewpoint article, Mario Clerici and Gene Shearer examined the role of T helper 1 (***Th1***)- and ***Th2*** -type responses in immune dysregulation associated with ***human*** ***immunodeficiency*** ***virus*** (***HIV***) infection. In this article, they consider the complications of a ***Th1*** - ***Th2*** model raised by the nomenclature, discuss the issue of cytokine production by non-T cells, and compare data obtained from T-cell clones with heterogeneous populations of leukocytes from patients. They define Th-cell responses and cytokine profiles as 'type 1' and 'type 2', and reemphasize the importance of strong cellular immune responses, along with the cytokines that augment and maintain such responses, in protective immunity against ***HIV*** infection and AIDS progression. Finally, they present a model of activation-induced, cytokine-modulated, programmed cell death as a major factor in the pathogenesis of ***HIV*** infection and AIDS.

L27 ANSWER 175 OF 185 MEDLINE
95232493 Document Number: 95232493. PubMed ID: 7716511. AIDS research. Cytokines move from the margins into the spotlight. Balter M. SCIENCE, (1995 Apr 14) 268 (5208) 205-6. Journal code: UJ7; 0404511. ISSN: 0036-8075. Pub. country: United States. Language: English.

L27 ANSWER 156 OF 185 MEDLINE
96285771 Document Number: 96285771. PubMed ID: 8724835. Cytokines in immune ***regulation*** /pathogenesis in ***HIV*** infection. Shearer G M; Clerici M; Sarin A; Berzofsky J A; Henkart P A. (National Cancer Institute, National Institutes of Health, Bethesda, MD 20892, USA.) CIBA FOUNDATION SYMPOSIUM, (1995) 195 142-7; discussion 147-53. Ref: 44. Journal code: D7X; 0356636. ISSN: 0300-5208. Pub. country: Netherlands. Language: English.

AB Two hallmarks of immunopathogenesis in the progression of ***HIV*** -infected individuals to AIDS are the loss of T helper (Th) cell function in response to antigens and the critical reduction in CD4+ T cell numbers. It is probable that these two phenomena are related. We observed that: (1) the failure to detect antigen-stimulated Th cell responses in vitro correlates with increased pokeweed mitogen/staphylococcal enterotoxin B (P/S)-stimulated and antigen-stimulated T cell death; and (2) both of these events are similarly modulated by immunoregulatory cytokines. Interleukin 2 (IL-2) and IL-12 (***Th1*** -type cytokines), as well as antibodies to IL-4 and IL-10 (which are ***Th2*** -type cytokines) restore in vitro Th cell responses to recall antigens such as influenza virus and ***HIV*** envelope synthetic peptides (env). P/S-induced T cell death affects both CD4+ and CD8+ T cell subsets, whereas death induced by stimulation with env affects only CD4+ T cells. In both examples, ***Th1*** -type cytokines and antibodies to ***Th2*** -type cytokines protect against T cell death. In contrast, IL-4 and IL-10 do not protect against death, and anti-IL-12 antibody can enhance T cell death. Our findings indicate that the loss of Th cell function and increased T cell death seen in vitro are correlated, and that in vivo ***HIV*** infection gives rise to inappropriate cytokines resulting in immune dysfunction and immunopathogenesis.

L27 ANSWER 177 OF 185 MEDLINE
95125467 Document Number: 95125467. PubMed ID: 7824955. ***TH2*** downregulation of macrophage ***HIV*** -1 replication. Montaner L J; Gordon S. SCIENCE, (1995 Jan 27) 267 (5197) 538-9. Journal code: UJ7; 0404511. ISSN: 0036-8075. Pub. country: United States. Language: English.

L27 ANSWER 164 OF 185 MEDLINE
96074662 Document Number: 96074662. PubMed ID: 7479952. Effects of

TH1 and ***TH2*** cytokines on CD8+ cell response against ***human*** ***immunodeficiency*** ***virus*** : implications for long-term survival. Barker E; Mackewicz C E; Levy J A. (Cancer Research Institute, University of California, San Francisco 94143-0128, USA.) PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1995 Nov 21) 92 (24) 11135-9. Journal code: PV3; 7505876. ISSN: 0027-8424. Pub. country: United States. Language: English.

AB CD8+ cells from long-term survivors [LTS; infected with ***human*** ***immunodeficiency*** ***virus*** (***HIV***) for 10 or more years and having CD4+ cell counts of > or = 500 cells per microliters] have a 3-fold greater ability to suppress ***HIV*** replication than do CD8+ cells from patients who have progressed to disease (progressors) during the same time period. A change in the pattern of cytokines produced in the host from those that typically favor cell-mediated immunity (T helper 1, ***TH1*** or type 1) to those that down-regulate it (T helper 2, ***TH2*** or type 2) was investigated as a cause of this reduced CD8+ cell anti- ***HIV*** function. ***Treatment*** of CD8+ cells from LTS with the ***TH1*** cytokine interleukin (IL)-2 enhanced their anti- ***HIV*** activity, whereas exposure of these cells to ***TH2*** cytokines IL-4 or IL-10 reduced their ability to suppress ***HIV*** replication and to produce IL-2. IL-2 could prevent and reverse the inhibitory effects of IL-4 and IL-10. Moreover, prolonged exposure of CD8+ cells from some progressors to IL-2 improved the ability of these cells to suppress ***HIV*** replication. These observations support previous findings suggesting that strong CD8+ cell responses play an important role in maintaining an asymptomatic state in ***HIV*** infection. The data suggest that the loss of CD8+ cell suppression of ***HIV*** replication associated with disease progression results from a shift in cytokine production within the infected host from a ***TH1*** to a ***TH2*** pattern. ***Modulation*** of these cytokines could provide benefit to ***HIV*** -infected individuals by improving their CD8+ cell anti- ***HIV*** activity.

L27 ANSWER 127 OF 185 MEDLINE
97381156 Document Number: 97381156. PubMed ID: 9238512. Role of cellular immunity in protection against ***HIV*** infection. Rowland-Jones S; Tan R; McMichael A. (Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford, United Kingdom.) ADVANCES IN IMMUNOLOGY, (1997) 65 277-346. Ref: 381. Journal code: 2N9; 0370425. ISSN: 0065-2776. Pub. country: United States. Language: English.

L27 ANSWER 119 OF 185 MEDLINE
1998131999 Document Number: 98131999. PubMed ID: 9472657. ***HIV*** -induced IL-6/IL-10 dysregulation of CD4 cells is associated with defective B cell help and autoantibody formation against CD4 cells. Weimer R; Zipperle S; Daniel V; Zimmermann R; Schimpf K; Opelz G. (Institute of Immunology, University of Heidelberg, Germany.) CLINICAL AND EXPERIMENTAL IMMUNOLOGY, (1998 Jan) 111 (1) 20-9. Journal code: DD7; 0057202. ISSN: 0009-9104. Pub. country: ENGLAND: United Kingdom. Language: English.

AB To analyse CD4 cell cytokine secretion and helper/suppressor function at a clonal level we established 446 CD4+ T cell clones (TCC) in four healthy controls, three ***HIV*** - haemophilia patients, four CDC II,III and four CDC IV patients. Spontaneous TCC secretion of ***Th1*** cytokines (IL-2, interferon-gamma (IFN-gamma)) and ***Th2*** cytokines (IL-4, IL-6, IL-10) was determined by ELISA. TCC helper and suppressor functions were tested in a pokeweed mitogen (PWM)-stimulated allogeneic co-culture system using a reverse haemolytic plaque assay for assessment of B cell responses. There was a significant association of TCC surface marker expression (Leu-8, CD45RA) with TCC IL-6 secretion in healthy controls (P

< 0.01), ***HIV*** - patients (P < or = 0.001) and CDC II,III patients (P < or = 0.01) but not in CDC IV patients. Likewise, TCC expression of Leu-8 and CD45RA was significantly associated with TCC suppressor function in healthy controls (P < or = 0.0005) but not in ***HIV*** -infected patients. A reduced TCC helper frequency (< or = 10% of TCC) and an enhanced TCC suppressor frequency (> 80% of TCC) were detected only in those ***HIV*** -infected patients who showed an excessively increased TCC IL-6 secretion (> 70% of TCC) together with a significantly diminished TCC IL-10 secretion (< or = 10% of TCC). CD4 cell autoantibodies also were found only in patients with this type of cytokine dysregulation. These data indicate that CD4 cell surface markers lose their functional relevance in ***HIV*** -infected patients. ***HIV*** -induced IL-6/IL-10 dysregulation of CD4+ T cells, i.e. the up- ***regulation*** of spontaneous IL-6 and down- ***regulation*** of spontaneous IL-10 secretion, appears to be involved in inducing CD4 helper defects and may promote autoantibody formation against CD4 cells.

L27 ANSWER 113 OF 185 MEDLINE
1998208295 Document Number: 98208295. PubMed ID: 9548515. Priming with IL-4 and IL-13 during ***HIV*** -1 infection restores in vitro IL-12 production by mononuclear cells of ***HIV*** -infected patients. Marshall J D; Robertson S E; Trinchieri G; Chehimi J. (The Wistar Institute of Anatomy and Biology, Philadelphia, PA 19104, USA.) JOURNAL OF IMMUNOLOGY, (1997 Dec 1) 159 (11) 5705-14. Journal code: IFB; 2985117R. ISSN: 0022-1767. Pub. country: United States. Language: English.

AB The production of proinflammatory cytokines can be regulated by several factors that exert activating or inhibitory effects. IL-4, IL-10, IL-13, TGF-beta, and PGE2 have demonstrated a very wide range of potent macrophage-deactivating activities and, specifically, down- ***regulation*** of the production of many proinflammatory monokines. IL-12 plays a key role during immune response by providing a link between natural resistance and adaptive immunity. We and others have previously shown an impairment in IL-12 production by PBMC from ***HIV*** -1-infected individuals in response to various stimuli, but defining the mechanism responsible remains elusive. In this study, we observed that pretreatment of PBMC from patients with IL-4 or IL-13 for 24 h primes the cells for enhanced production of IL-12 in response to Staphylococcus aureus, and almost completely restores their deficient IL-12 production when compared with healthy controls. Although this priming effect was completely abrogated by IL-10 and PGE2, IL-10 was produced equivalently by untreated and IL-4- or IL-13-pretreated PBMC from both patients and controls. Additionally, indomethacin, which shuts off PGE2 synthesis, and cAMP-blocking reagents failed to restore or enhance IL-12 production. The priming effect of IL-4 and IL-13 is at the transcription level for both p40 and p35 genes. This complete restoration of IL-12 production by ***Th2*** -associated cytokines was unexpected in light of the mutually antagonistic roles of IL-12 and IL-4 in promoting ***Th1*** or ***Th2*** immune responses.

L27 ANSWER 87 OF 185 MEDLINE
1999217474 Document Number: 99217474. PubMed ID: 10202824. Persistent alterations in T-cell repertoire, cytokine and chemokine receptor gene expression after 1 year of highly active antiretroviral ***therapy*** . Martinon F; Michelet C; Peguillet I; Taoufik Y; Lefebvre P; Goujard C; Guillet J G; Delfraissy J F; Lantz O. (ICGM-INSERM U445, Hopital Cochin, Paris, France.) AIDS, (1999 Feb 4) 13 (2) 185-94. Journal code: AID; 8710219. ISSN: 0269-9370. Pub. country: ENGLAND: United Kingdom. Language: English.

AB OBJECTIVES: To examine T-cell repertoire modifications, the evolution of

T-helper (TH)1/ ***TH2*** cytokine imbalance and modifications in chemokine receptor expression when the viral load is decreased by 2-3 log10 copies/ml under highly active antiretroviral ***therapy*** (HAART). DESIGN: Sixteen patients previously treated with zidovudine and lamivudine, with CD4 cells below 300 x 10(6)/l and viraemia above 30000 copies/ml were treated by saquinavir and ritonavir together with both reverse transcriptase (RT) inhibitors (ANRS 069 trial). T-cell repertoire, chemokine receptor and lymphokine expression were studied from peripheral blood mononuclear cells sampled at weeks 0, 24 and 48. METHODS: T-cell repertoire study was carried out using the Immunoscope method. Interleukin (IL)-12 receptor beta2, CC-chemokine receptor (CCR)-3, CXC-chemokine receptor-4 and CCR-5 expression in CD4+ cells was measured by kinetic quantitative PCR and IL-2, IL-4, IL-10, IL-13, interferon (IFN)-gamma were measured using a quantitative RT-PCR assay with homologous internal standards. RESULTS: Repertoire alterations were more frequent in CD4- than in CD4+ cells and persisted despite undetectable viraemia. Increased CCR-3 expression and spontaneous IFN-gamma as well as mitogenic induced IL-13 were observed at baseline and decreased slightly under HAART. CONCLUSION: The CD8+ cell repertoire alterations were profound, whereas the CD4+ cell alterations were moderate and both persisted unchanged under HAART. The ***TH1*** / ***TH2*** imbalance was more related to ***TH2*** over-expression than to ***TH1*** deficiency and persisted for at least 1 year under HAART.

L29 ANSWER 2 OF 2 MEDLINE

94294789 Document Number: 94294789. PubMed ID: 8023143. Lack of evidence for the dichotomy of ***TH1*** and ***TH2*** predominance in HIV-infected individuals. Graziosi C; Pantaleo G; Gantt K R; Fortin J P; Demarest J F; Cohen O J; Sekaly R P; ***Fauci A S*** . (Laboratory of Immunoregulation, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD 20892.) SCIENCE, (1994 Jul 8) 265 (5169) 248-52. Journal code: UJ7; 0404511. ISSN: 0036-8075. Pub. country: United States. Language: English.

AB A switch from a T helper 1 (***TH1***) cytokine phenotype to a ***TH2*** phenotype has been proposed as a critical element in the progression of human immunodeficiency virus (HIV) disease. Here, constitutive cytokine expression was analyzed in unfractionated and sorted cell populations isolated from peripheral blood and lymph nodes of HIV-infected individuals at different stages of disease. Expression of interleukin-2 (IL-2) and IL-4 was barely detectable (or undetectable) regardless of the stage of disease. CD8+ cells expressed large amounts of interferon gamma and IL-10, and the levels of these cytokines remained stably high throughout the course of infection. Furthermore, similar patterns of cytokine expression were observed after stimulation in vitro of purified CD4+ T cell populations obtained from HIV-infected individuals at different stages of disease. These results indicate that a switch from the ***TH1*** to the ***TH2*** cytokine phenotype does not occur during the progression of HIV disease.

L33 ANSWER 2 OF 11 MEDLINE

97420772 Document Number: 97420772. PubMed ID: 9275214. Evidence for rapid disappearance of initially expanded HIV-specific CD8+ T cell clones during primary HIV infection. Pantaleo G; Soudeyns H; Demarest J F; Vaccarezza M; Graziosi C; Paolucci S; Daucher M; Cohen O J; Denis F; Biddison W E; Sekaly R P; ***Fauci A S*** . (Laboratory of Immunoregulation, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD 20892, USA.. Giuseppe.Pantaleo@chuv.hospvd.ch) . PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1997 Sep 2) 94 (18) 9848-53. Journal code: PV3; 7505876. ISSN: 0027-8424. Pub. country: United States.

Language: English.

AB Down-regulation of the initial burst of viremia during primary HIV infection is thought to be mediated predominantly by HIV-specific cytotoxic T lymphocytes, and the appearance of this response is associated with major perturbations of the ***T*** ***cell*** ***receptor*** repertoire. Changes in the ***T*** ***cell*** ***receptor*** repertoire of virus-specific cytotoxic T lymphocytes were analyzed in patients with primary infection to understand the failure of the cellular immune response to control viral spread and replication. This analysis demonstrated that a significant number of HIV-specific T cell clones involved in the primary immune response rapidly disappeared. The disappearance was not the result of mutations in the virus epitopes recognized by these clones. Evidence is provided that phenomena such as high-dose tolerance or clonal exhaustion might be involved in the disappearance of these monoclonally expanded HIV-specific cytotoxic T cell clones. These findings should provide insights into how HIV, and possibly other viruses, elude the host immune response during primary infection.

L33 ANSWER 5 OF 11 MEDLINE
96201239 Document Number: 96201239. PubMed ID: 8607594. Immunopathogenic mechanisms of HIV infection. ***Fauci A S*** ; Pantaleo G; Stanley S; Weissman D. (National Institutes of Health, Bethesda, Maryland, USA.) ANNALS OF INTERNAL MEDICINE, (1996 Apr 1) 124 (7) 654-63. Ref: 56. Journal code: 5A6; 0372351. ISSN: 0003-4819. Pub. country: United States. Language: English.

AB A complex array of multiphasic and multifactorial immunopathogenic mechanisms are involved in the establishment and progression of human immunodeficiency virus (HIV) disease. After primary infection, acute viremia occurs with wide dissemination of HIV. During this early viremic phase, the virus is trapped within the processes of follicular dendritic cells in the germinal centers of lymphoid tissue. Also, during this phase of primary infection, some patients show major expansions of certain subsets of CD8+ T cells that are identified by the expression of a particular variable region of the beta chain of the ***T*** - ***cell*** ***receptor*** . These expansions are manifestations of responses to HIV that may be important in controlling the progression of HIV infection. In addition, inappropriate immune activation and elevated secretion of certain proinflammatory cytokines occur during HIV infection; these cytokines play a role in the regulation of HIV expression in the tissues. Infection of progenitor cells in bone marrow and the thymus contribute to the lack of regeneration of immunocompetent cells. Dendritic cells are involved in the initiation and propagation of HIV infection in CD4+ T cells. In studies of long-term nonprogressors - persons who have stable CD4+ T-cell counts and no HIV disease progression despite years of HIV infection - preserved lymph node architecture, low viral burden, and viral expression were found.

L31 ANSWER 3 OF 62 MEDLINE
1999432163 Document Number: 99432163. PubMed ID: 10500107. Latent reservoirs of HIV: obstacles to the eradication of virus. Chun T W; ***Fauci A S*** . (Laboratory of Immunoregulation, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD 20892, USA.. twchun@nih.gov) . PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1999 Sep 28) 96 (20) 10958-61. Journal code: PV3; 7505876. ISSN: 0027-8424. Pub. country: United States. Language: English.

AB The use of highly active antiretroviral therapy (HAART) in the treatment of HIV-1-infected individuals has provided a considerable amount of

information regarding the dynamics of viral replication and has resulted in enormous advances in HIV therapeutics. The profound suppression of plasma viremia in HIV-infected individuals receiving HAART has resulted in a highly beneficial clinical effect and a dramatic decrease in the death rate attributable to AIDS. Nonetheless, the persistance of reservoirs of HIV, including latently infected, resting CD4+ T cells that can give rise to infectious HIV upon stimulation in vitro, has posed a sobering challenge to the long-term control or eradication of HIV in infected individuals receiving HAART. Although a recent study has demonstrated th at the size of the pool of latently infected, resting CD4+ T cells can be markedly diminished with intermittent interleukin (***IL*** - ***2***) and continuous HAART, complete eradication of HiV in infected individuals remains extremely problematic. Here we discuss recent developments in studies of the latent reservoir of HIV in patients receiving HAART and implications for the long-term treatment of infected individuals and eradication of the infection.

L31 ANSWER 4 OF 62 MEDLINE
1999297913 Document Number: 99297913. PubMed ID: 10371503. Effect of interleukin-2 on the pool of latently infected, resting CD4+ T cells in HIV-1-infected patients receiving highly active anti-retroviral therapy. Chun T W; Engel D; Mizell S B; Hallahan C W; Fischette M; Park S; Davey R T Jr; Dybul M; Kovacs J A; Metcalf J A; Mican J M; Berrey M M; Corey L; Lane H C; ***Fauci A S*** . (Laboratory of Immunoregulation, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland 20892, USA.. twchun@nih.gov) . NATURE MEDICINE, (1999 Jun) 5 (6) 651-5. Journal code: CG5; 9502015. ISSN: 1078-8956. Pub. country: United States. Language: English.

AB The size of the pool of resting CD4+ T cells containing replication-competent HIV in the blood of patients receiving intermittent interleukin (***IL***)- ***2*** plus highly active anti-retroviral therapy (HAART) was significantly lower than that of patients receiving HAART alone. Virus could not be isolated from the peripheral blood CD4+ T cells in three patients receiving ***IL*** - ***2*** plus HAART, despite the fact that large numbers of resting CD4+ T cells were cultured. Lymph node biopsies were done in two of these three patients and virus could not be isolated. These results indicate that the intermittent administration of ***IL*** - ***2*** with continuous HAART may lead to a substantial reduction in the pool of resting CD4+ T cells that contain replication-competent HIV.

L31 ANSWER 5 OF 62 MEDLINE
1998317020 Document Number: 98317020. PubMed ID: 9653086. Induction of HIV-1 replication in latently infected CD4+ T cells using a combination of cytokines. Chun T W; Engel D; Mizell S B; Ehler L A; ***Fauci A S*** . (Laboratory of Immunoregulation, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland 20892, USA.. twchun@nih.gov) . JOURNAL OF EXPERIMENTAL MEDICINE, (1998 Jul 6) 188 (1) 83-91. Journal code: I2V; 2985109R. ISSN: 0022-1007. Pub. country: United States. Language: English.

AB Although it has been demonstrated that certain cytokines, particularly proinflammatory cytokines, can enhance ongoing viral replication in peripheral blood mononuclear cells (PBMCs) of HIV-1-infected individuals, it is unclear what role these cytokines play in the induction of HIV-1 replication in latently infected, resting CD4(+) T cells. This study demonstrates that the in vitro combination of the proinflammatory cytokines interleukin (IL)-6 and tumor necrosis factor (TNF)-alpha together with the immunoregulatory cytokine ***IL*** - ***2*** are potent inducers of viral replication in highly purified, latently

infected, resting CD4+ T cells derived from HIV-infected individuals who are antiretroviral therapy-naive as well as those who are receiving highly active antiretroviral therapy (HAART). Viral replication induced by this combination of cytokines was completely suppressed in the presence of HAART in vitro. Given that an array of cytokines, including IL-6, TNF-alpha, and ***IL*** - ***2*** , are copiously expressed in the microenvironment of the lymphoid tissues, which harbor the latent viral reservoirs, induction of HIV by this combination of cytokines may in part explain the commonly observed reappearance of detectable plasma viremia in HIV-infected individuals in whom HAART was discontinued. Moreover, since it is likely that these infected cells die upon activation of virus and that HAART prevents spread of virus to adjacent cells, the observation that this combination of cytokines can markedly induce viral replication in this reservoir may have important implications for the activation-mediated diminution of the latent reservoir of HIV in patients receiving HAART.

L31 ANSWER 13 OF 62 MEDLINE
96320760 Document Number: 96320760. PubMed ID: 8739561. Interleukin-2 and human immunodeficiency virus infection: pathogenic mechanisms and potential for immunologic enhancement. Kinter A; ***Fauci A S*** . (Laboratory of Immunoregulation, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Md, USA.) IMMUNOLOGIC RESEARCH, (1996) 15 (1) 1-15. Ref: 136. Journal code: IMR; 8611087. ISSN: 0257-277X. Pub. country: United States. Language: English.

AB A hallmark of human immunodeficiency virus (HIV) infection is the progressive loss of CD4+ T lymphocytes; however, qualitative defects in immune responses occur prior to the precipitous drop CD4+ T cell numbers. One of the first immunologic defects to be described in HIV-infected individuals is a deficiency in interleukin (***IL***)- ***2*** production. The addition of ***IL*** - ***2*** in vitro to cultures of mononuclear cells from HIV-infected individuals partially or completely restored certain defective cellular immune responses. However, production of or addition of ***IL*** - ***2*** has also been associated with increased viral replication in infected T cells. These observations underscore the pernicious correlation between immune activation and HIV replication. However, recent in vitro and in vivo studies have provided promising preliminary results suggesting that, at least at certain stages of disease, the benefits of ***IL*** - ***2*** mediated immune enhancement may outweigh or override the inductive effects of this cytokine on HIV production.

L31 ANSWER 14 OF 62 MEDLINE
96210653 Document Number: 96210653. PubMed ID: 8633076. Kinetics of cytokine expression during primary human immunodeficiency virus type 1 infection. Graziosi C; Gantt K R; Vaccarezza M; Demarest J F; Daucher M; Saag M S; Shaw G M; Quinn T C; Cohen O J; Welbon C C; Pantaleo G; ***Fauci A S*** . (Laboratory of Immunoregulation, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD 20892-1876, USA.) PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1996 Apr 30) 93 (9) 4386-91. Journal code: PV3; 7505876. ISSN: 0027-8424. Pub. country: United States. Language: English.

AB In the present study, we have determined the kinetics of constitutive expression of a panel of cytokines [interleukin (***IL***) ***2*** , ***IL*** - ***4*** , IL-6, ***IL*** - ***10*** , interferon gamma (IFN-gamma), and tumor necrosis factor alpha (TNF-alpha)] in sequential peripheral blood mononuclear cell samples from nine individuals with primary human immunodeficiency virus infection. Expression of

IL - ***2*** and ***IL*** - ***4*** was barely detected in peripheral blood mononuclear cells. However, substantial levels of ***IL*** - ***2*** expression were found in mononuclear cells isolated from lymph node. Expression of IL-6 was detected in only three of nine patients, and IL-6 expression was observed when transition from the acute to the chronic phase had already occurred. Expression of ***IL*** - ***10*** and TNF-alpha was consistently observed in all patients tested, and levels of both cytokines were either stable or progressively increased over time. Similar to ***IL*** - ***10*** and TNF-alpha, IFN-gamma expression was detected in all patients; however, in five of nine patients, IFN-gamma expression peaked very early during primary infection. The early peak in IFN-gamma expression coincided with oligoclonal expansions of CD8+ T cells in five of six patients, and CD8+ T cells mostly accounted for the expression of this cytokine. These results indicate that high levels of expression of proinflammatory cytokines are associated with primary infection and that the cytokine response during this phase of infection is strongly influenced by oligoclonal expansions of CD8+ T cells.

L31 ANSWER 16 OF 62 MEDLINE
95353764 Document Number: 95353764. PubMed ID: 7627621. ***IL*** - ***10*** synergizes with multiple cytokines in enhancing HIV production in cells of monocytic lineage. Weissman D; Poli G; ***Fauci A S*** . (Laboratory of Immunoregulation, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, MD 20892, USA.) JOURNAL OF ACQUIRED IMMUNE DEFICIENCY SYNDROMES AND HUMAN RETROVIROLOGY, (1995 Aug 15) 9 (5) 442-9. Journal code: B7J; 9501482. ISSN: 1077-9450. Pub. country: United States. Language: English.

AB Several cytokines, whose expression is increased in human immunodeficiency virus (HIV)-infected individuals, can enhance virus replication in CD4+ T lymphocytes and mononuclear phagocytes (MP). We have previously reported that interleukin (***IL***)- ***10*** inhibited HIV replication in acutely infected monocyte-derived macrophages (MDM) at concentrations that completely blocked the production of endogenous tumor necrosis factor-alpha (TNF-alpha) and IL-6 from infected cells. In the present study, lower concentrations of ***IL*** - ***10*** , which were unable to completely suppress endogenous cytokines, paradoxically enhanced HIV replication in MDM induced by other cytokines. This synergistic induction of HIV expression by ***IL*** - ***10*** in combination with TNF-alpha, IL-6, and other cytokines was also observed in the chronically infected promonocytic cell line, U1. The enhancing effect of ***IL*** - ***10*** was correlated with an increase in HIV mRNA accumulation and potentiation of phorbol ester-induced long terminal repeat-driven transcription that was independent of the NF-kappa B and Sp1 transcription factors. Thus, ***IL*** - ***10*** is a cytokine capable of exerting complex regulatory effects on HIV expression in MP as a function of its own concentration and of the presence of other HIV regulatory cytokines.

L31 ANSWER 18 OF 62 MEDLINE
95151356 Document Number: 95151356. PubMed ID: 7848677. Interleukin 10 blocks HIV replication in macrophages by inhibiting the autocrine loop of tumor necrosis factor alpha and interleukin 6 induction of virus. Weissman D; Poli G; ***Fauci A S*** . (Laboratory of Immunoregulation, National Institutes of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland 20892.) AIDS RESEARCH AND HUMAN RETROVIRUSES, (1994 Oct) 10 (10) 1199-206. Journal code: ART; 8709376. ISSN: 0889-2229. Pub. country: United States. Language: English.

AB Human interleukin 10 is a pleiotropic cytokine capable of suppressing

cytokine production from macrophages and T cells; in addition, it exerts complex regulatory effects on CD8+ T cells, natural killer cells, vascular endothelial cells, and B lymphocytes. Levels of ***IL*** - ***10*** are elevated in HIV-infected individuals, suggesting that this cytokine may play a role in the suppression of T cell and monocyte/macrophage function typical of HIV disease. In this article, ***IL*** - ***10*** blocked HIV-induced tumor necrosis factor alpha and interleukin 6 secretion and inhibited HIV replication in monocyte-derived macrophages (MDMs). The inhibition by ***IL*** - ***10*** was correlated with a block in endogenous TNF-alpha and IL-6 secretion from HIV-infected MDMs.

L34 ANSWER 32 OF 33 MEDLINE
94294788 Document Number: 94294788. PubMed ID: 8023142. Ability of ***HIV*** to promote a ***TH1*** to ***TH0*** shift and to replicate preferentially in ***TH2*** and ***TH0*** cells. Maggi E; Mazzetti M; Ravina A; Annunziato F; de Carli M; Piccinni M P; Manetti R; Carbonari M; Pesce A M; del Prete G; +. (Division of Clinical Immunology and Allergy, University of Florence, Italy.) SCIENCE, (1994 Jul 8) 265 (5169) 244-8. Journal code: UJ7; 0404511. ISSN: 0036-8075. Pub. country: United States. Language: English.

AB Both interferon gamma (IFN-gamma) produced by T helper 1 (***TH1***) lymphocytes and interleukin-4 (IL-4) produced by ***TH2*** lymphocytes were reduced in either bulk circulating mononuclear cells or mitogen-induced CD4+ T cell clones from the peripheral blood of individuals infected with ***human*** ***immunodeficiency*** ***virus*** (***HIV***). There was a preferential reduction in clones producing IL-4 and IL-5 in the advanced phases of infection. However, enhanced proportions of CD4+ T cell clones producing both ***TH1*** -type and ***TH2*** -type cytokines (***TH0*** clones) were generated from either skin-infiltrating T cells that had been activated in vivo or peripheral blood T cells stimulated by antigen in vitro when cells were isolated from ***HIV*** -infected individuals. All ***TH2*** and most ***TH0*** clones supported viral replication, although viral replication was not detected in any of the ***TH1*** clones infected in vitro with ***HIV*** . These results suggest that ***HIV*** (i) does not induce a definite ***TH1*** to ***TH2*** switch, but can favor a shift to the ***TH0*** phenotype in response to recall antigens, and (ii) preferentially replicates in CD4+ T cells producing ***TH2*** -type cytokines (***TH2*** and ***TH0***).

L34 ANSWER 31 OF 33 MEDLINE
95000921 Document Number: 95000921. PubMed ID: 7917511. An alternative view of the ***Th1*** / ***Th2*** switch hypothesis in ***HIV*** infection. Romagnani S; Maggi E; Del Prete G. (Division of Allergology and Clinical Immunology, Istituto di Clinica Medica III, University of Florence, Italy.) AIDS RESEARCH AND HUMAN RETROVIRUSES, (1994 May) 10 (5) iii-ix. Ref: 49. Journal code: ART; 8709376. ISSN: 0889-2229. Pub. country: United States. Language: English.

AB A theory that seeks to explain what induces the relentless progression of ***HIV*** -infected subjects to AIDS has received considerable attention. This theory holds that ***HIV*** infection results in a ***Th1*** / ***Th2*** switch. However, analysis of constitutive cytokine mRNA expression in lymphoid tissues from ***HIV*** -infected individuals did not confirm an in vivo ***Th1*** / ***Th2*** switch. Moreover, data available at the level of in vitro-stimulated peripheral blood mononuclear cells or cloned T cells do not provide clear evidence for a definite switch to the ***Th2*** responses in any ***HIV*** -infected subject and in any phase of ***HIV*** infection. At most, currently

available data on the profile of cytokines released in response to in vitro stimulation suggest a ***Th1*** -to- ***Th0*** shift in a proportion of memory CD4+ T cells. On the other hand, experiments of in vitro infection with ***HIV*** of already established CD4+ T cell clones indicated that ***Th2*** and ***Th0*** cells support ***HIV*** replication better than ***Th1*** cells, suggesting that early destruction of ***Th2*** cells by direct or indirect ***HIV*** -mediated cell killing may occur. Finally, in some ***HIV*** -infected individuals with low CD4+ T cell counts, a prevalence of CD8+ T cells producing type 2 cytokines was found in both peripheral blood and skin. Thus, although the induction of a general ***Th2*** state in ***HIV*** infection is not proven, enhanced production of type 2 cytokines may occur in a proportion of ***HIV*** -infected individuals and play some role in the pathogenesis of the disease.

L34 ANSWER 29 OF 33 MEDLINE
95122085 Document Number: 95122085. PubMed ID: 7821929. Role of ***TH1*** / ***TH2*** cytokines in ***HIV*** infection. Romagnani S; Del Prete G; Manetti R; Ravina A; Annunziato F; De Carli M; Mazzetti M; Piccinni M P; D'Elios M M; Parronchi P; +. (Department of Allergy & Clinical Immunology, University of Florence, Italy.) IMMUNOLOGICAL REVIEWS, (1994 Aug) 140 73-92. Ref: 65. Journal code: GG4; 7702118. ISSN: 0105-2896. Pub. country: Denmark. Language: English.

AB Different experimental approaches were used to prove or disprove the " ***TH1*** / ***TH2*** switch theory" of ***HIV*** -infection. No increase, or even a decrease, in the production of ***TH2*** -type cytokines (IL-4, IL-5, and IL-10) by either bulk circulating mononuclear cells or CD4+ T-cell clones generated by PHA stimulation of single T cells from ***HIV*** -infected individuals in all stages of disease compared to ***HIV*** -negative donors was observed. However, enhanced proportions of CD4+ T-cell clones able to produce both ***TH1*** -type and ***TH2*** -type cytokines (***TH0*** clones) were derived from either skin-infiltrating, in vivo-activated, T cells or in vitro antigen-stimulated peripheral blood T cells of ***HIV*** -infected individuals. Of note, ***TH1*** , ***TH2*** and ***TH0*** clones obtained from ***HIV*** -seronegative healthy donors showed different ability to support viral replication after infection with ***HIV*** in vitro. All ***TH2*** and most ***TH0*** clones supported ***HIV*** replication efficiently, whereas ***TH1*** clones did not. These results suggest preferential ***HIV*** replication in T cells producing ***TH2*** -type cytokines rather than ***TH1*** / ***TH2*** switch in ***HIV*** infection.

L34 ANSWER 22 OF 33 MEDLINE
96332554 Document Number: 96332554. PubMed ID: 8706325. CD8+ lymphocyte phenotype and cytokine production in long-term non-progressor and in progressor patients with ***HIV*** -1 infection. Zanussi S; Simonelli C; D'Andrea M; Caffau C; Clerici M; Tirelli U; DePaoli P. (Department of Microbiology-Immunology-Virology, C.R.O. Aviano, Italy.) CLINICAL AND EXPERIMENTAL IMMUNOLOGY, (1996 Aug) 105 (2) 220-4. Journal code: DD7; 0057202. ISSN: 0009-9104. Pub. country: ENGLAND: United Kingdom. Language: English.

AB In most ***HIV*** -1-infected patients, clinical and immunological progression develops within a few years. Few infected people, termed long-term non-progressors (LTNP), remain healthy and immunologically stable for a long time. The factors governing the maintenance of this condition are not well known, but it is conceivable that CD8+ lymphocytes, cells that play a central role in controlling in vitro ***HIV*** replication, may have a part in vivo in this process. The aim of this

study was to characterize the phenotypic profile and the cytokine production of CD8+ cells in a group of LTNP patients who had stable CD4+ cell counts (> 500/mm3) for at least 7 years. Their CD8+ absolute numbers were similar to a control group composed of ***HIV*** -1+ patients who have a progressive decline of their CD4+ cell counts. However, our multiparameter immunofluorescence studies show that a clinical and immunologically stable condition is associated with the presence of a CD28+, CD95 strongly positive CD8+ population, while disease progression is marked by the CD28-CD95+CD8+ subset. Purified CD8+ cells from LTNP retain their ability to produce IL-2, interferon-gamma (IFN-gamma) and, to a lesser degree, to produce IL-10 and IL-4. In contrast, CD8+ cells from progressors are unable to secrete IL-2 and IL-10. Although CD8+ cytokine profile does not fit with the proposed T helper (Th)1/ ***Th2*** switch in progressive ***HIV*** infection, LTNP CD8+ T cells maintain their capacity to produce IL-2 and IL-10 (***Th0*** -like), a pattern very similar to that observed in normal ***HIV*** healthy controls. We suggest that CD8+ cells expressing CD28, CD95 and having a ***Th0*** -like profile may be considered to be associated with long-term survival.

L36 ANSWER 4 OF 77 MEDLINE
2001469289 Document Number: 21405432. PubMed ID: 11514956. Different rates of CD4+ and CD8+ T-cell proliferation in ***interleukin*** - ***2*** -treated ***human*** ***immunodeficiency*** ***virus*** -positive subjects. Caggiari L; Zanussi S; Crepaldi C; Bortolin M T; Caffau C; D'Andrea M; De Paoli P. (Division of Microbiology, Immunology and Virology, Centro di Riferimento Oncologico, IRCCS, 33081 Aviano, Italy.) CYTOMETRY, (2001 Aug 15) 46 (4) 233-7. Journal code: D92; 8102328. ISSN: 0196-4763. Pub. country: United States. Language: English.

AB BACKGROUND: ***Interleukin*** - ***2*** (***IL*** - ***2***) has been used successfully to increase CD4 cell counts in patients who are ***human*** ***immunodeficiency*** ***virus*** (***HIV***) positive. The mechanisms involved in this phenomenon are unknown. We hypothesized that a differential proliferation rate of CD4+ compared with CD8+ lymphocytes could be related to the increase of CD4 counts and of CD4/CD8 ratios that occur in ***HIV*** + patients during ***IL*** - ***2*** treatment. METHODS: We enrolled in our study 14 ***HIV*** + patients treated with ***IL*** - ***2*** or with highly active antiretroviral therapy (HAART) during a 96-week observation period. Using flow cytometry, we measured longitudinally the expression of the Ki67 antigen in peripheral blood CD4+ and CD8+ lymphocyte subsets. RESULTS: Compared with HAART alone, ***IL*** - ***2*** produced a rapid increase of Ki67+ proliferating CD4 cells and a concomitant increase of the CD4/CD8 ratios, whereas the corresponding CD8 proliferation increased slightly. On the contrary, HAART alone was effective in suppressing equally both CD4 and CD8 proliferation. CONCLUSIONS: Our results suggest a selective activity of ***IL*** - ***2*** on CD4 T-cell proliferation; on the contrary, CD8-specific proliferation is affected minimally during treatment. This information may offer the potential to plan correctly immune activating regimens.

L36 ANSWER 6 OF 77 MEDLINE
2001414990 Document Number: 21357617. PubMed ID: 11465092. ***Interleukin*** - ***2*** induced immune effects in ***human*** ***immunodeficiency*** ***virus*** -infected patients receiving intermittent ***interleukin*** - ***2*** ***immunotherapy*** . Kovacs J A; Vogel S; Metcalf J A; Baseler M; Stevens R; Adelsberger J; Lempicki R; Hengel R L; Sereti I; Lambert L; Dewar R L; Davey R T Jr; Walker R E; Falloon J; Polis M A; Masur H; Lane H C. (Critical Care Medicine Department, Clinical Center, National Institutes of Health,

Bethesda, USA.. jkovacs@nih.gov) . EUROPEAN JOURNAL OF IMMUNOLOGY, (2001 May) 31 (5) 1351-60. Journal code: EN5; 1273201. ISSN: 0014-2980. Pub. country: Germany: Germany, Federal Republic of. Language: English.

AB To characterize the immunological effects of intermittent ***IL*** - ***2*** therapy, which leads to selective increases in CD4+ T lymphocytes in ***HIV*** -infected patients, 11 patients underwent extensive immunological evaluation. While ***IL*** - ***2*** induced changes in both CD4+ and CD8+ cell number acutely, only CD4+ cells showed sustained increases following discontinuation of ***IL*** - ***2*** . Transient increases in expression of the activation markers CD38 and HLA-DR were seen on both CD4+ and CD8+ cells, but CD25 (a chain of the ***IL*** - ***2*** receptor) increased exclusively on CD4+ cells. This increase in CD25 expression was sustained for months following discontinuation of ***IL*** - ***2*** , and was seen in naive as well as memory cells. ***IL*** - ***2*** induced cell proliferation, but tachyphylaxis to these proliferative effects developed after 1 week despite continued ***IL*** - ***2*** administration. It thus appears that sustained CD25 expression selectively on CD4+ cells is a critical component of the immunological response to ***IL*** - ***2*** , and that intermittent administration of ***IL*** - ***2*** is necessary to overcome the tachyphylaxis to ***IL*** - ***2*** -induced proliferation.

L36 ANSWER 10 OF 77 MEDLINE
2001363436 Document Number: 21317671. PubMed ID: 11424974. Low-dose daily ***interleukin*** - ***2*** ***immunotherapy*** : accelerating immune restoration and expanding ***HIV*** -specific T-cell immunity without toxicity. Smith K A. (Division of Immunology, Weill Medical College of Cornell University, New York, New York 10021, USA.. kasmith@med.cornell.edu) . AIDS, (2001 Feb) 15 Suppl 2 S28-35. Ref: 49. Journal code: AID; 8710219. ISSN: 0269-9370. Pub. country: England: United Kingdom. Language: English.

AB There is now a great deal of interest in therapies focused on improving the function of the immune system in the treatment of individuals infected with the ***HIV*** . Although the antiviral drugs effectively suppress replication of the virus, they cannot cure the infection. Therefore, it now appears that both antivirals and immune system stimulants will be necessary to maximally suppress residual latent virus, thereby allowing the discontinuation of the antivirals without relapse of detectable plasma virus. ***Interleukin*** - ***2*** (***IL*** - ***2***) the first cytokine to be discovered at the molecular level has been used as a therapeutic in ***HIV*** infection, because it is critical for a normal functioning immune response. ***IL*** - ***2*** is essential for the survival and proliferative expansion of antigen-activated T cells and natural killer (NK) cells, and also for promoting their differentiated functions of cytokine secretion and cytolysis. Howèver, as ***IL*** - ***2*** stimulates both the innate and acquired immune responses, when used as a therapeutic it can lead to severe toxicity when given in high doses. This review focuses on low dose, daily ***IL*** - ***2*** therapy, used to accelerate the recovery of the immune system when viral replication is suppressed maximally with antivirals. In addition, the principles of the use of ***IL*** - ***2*** to activate ***HIV*** -specific immune reactivity are discussed. At least two signals are required to promote the proliferative expansion and function of antiviral effector lymphocytes, ***HIV*** antigens and ***IL*** - ***2*** .

L36 ANSWER 11 OF 77 MEDLINE
2001317070 Document Number: 21285055. PubMed ID: 11392678. Improving immune function and controlling viral replication in ***HIV***

-1-infected patients with immune-based therapies. Angel J B. (Division of Infectious Diseases, Ottawa Hospital-General Campus, University of Ottawa, Ottawa.) AIDS Read, (2001 Apr) 11 (4) 209-21. Ref: 85. Journal code: DL5; 9206753. ISSN: 1053-0894. Pub. country: United States. Language: English.

AB Restoring and preserving immune function is a key component to successfully managing ***HIV*** -1 disease. Phase II/III studies have evaluated the safety and immunologic effects of immune-based therapies, including granulocyte-macrophage colony-stimulating factor, ***interleukin*** - ***2*** , and an inactivated ***HIV*** -1 immunogen, as adjuncts to antiretroviral therapy. Addition of each of these immune-based therapies to a background antiretroviral regimen enhanced, to varying degrees, immunologic function and suppression of viral replication in ***HIV*** -1-infected patients, suggesting a potential role for immune-based therapies in the treatment of ***HIV*** -1 disease. Further studies are needed to better characterize specific immunologic and virologic effects in different patient populations and to determine their impact on clinical outcomes.

L4 ANSWER 18 OF 20 MEDLINE
92194934 Document Number: 92194934. PubMed ID: 1347855. ***T*** - ***cell*** ***receptor*** variable gene products and early ***HIV*** -1 infection. Dalgleish A G; Wilson S; Gompels M; Ludlam C; Gazzard B; Coates A M; Habeshaw J. (Department of Cellular and Molecular Sciences, St George's Hospital Medical School, London, UK.) LANCET, (1992 Apr 4) 339 (8797) 824-8. Journal code: L0S; 2985213R. ISSN: 0140-6736. Pub. country: ENGLAND: United Kingdom. Language: English.

AB To assess the hypothesis that the ***human*** ***immunodeficiency*** ***virus*** (***HIV***) might mimic major histocompatibility complex (MHC) allodeterminants and interact with T-cell receptors (TCRs) of alloreactive T-cells, we have done a preliminary analysis of the range of alpha beta ***TCR*** gene products in 16 ***HIV*** -1-seropositive individuals with normal CD4 counts and in 16 healthy ***HIV*** -1-negative controls. Using a panel of monoclonal ***antibodies*** with a two-colour direct immunofluorescence method, we found a significant increase in the expression of the V beta 5.3 subfamily in the ***HIV*** -positive patient group compared with controls (p less than 0.01). Selected increase in expression of V beta sequences has been described in various autoimmune conditions and our findings raise the possibility that the ***immunopathological*** damage from ***HIV*** infection may be due to the induction of autoreactivity. If ***HIV*** does mimic MHC II, the normal immune response to the virus could represent an autoimmune process similar to graft-versus-host disease.

L4 ANSWER 16 OF 20 MEDLINE
93236722 Document Number: 93236722. PubMed ID: 8476511. Changes in the cytotoxic T-cell repertoire of ***HIV*** -1-infected individuals: relationship to disease progression. Grant M D; Smaill F M; Laurie K; Rosenthal K L. (Department of Pathology, McMaster University Health Sciences Centre, Hamilton, Ontario, Canada.) VIRAL IMMUNOLOGY, (1993 Spring) 6 (1) 85-95. Journal code: AD0; 8801552. ISSN: 0882-8245. Pub. country: United States. Language: English.

AB The repertoire of antigen-specific receptors expressed on T lymphocytes is shaped by fixed genetic and variable environmental selective pressures. Recent technological advances have enabled the analysis of ***T*** - ***cell*** ***receptor*** (***TCR***) expression in the context of selective pressures arising through normal immune system development and also through pathological features of disease. The pathological

features of acquired immune deficiency syndrome (AIDS) are reflected by selective depletion of particular T lymphocyte subsets and expansion of others. An important question concerning the ***immunopathogenesis*** of AIDS is whether or not the perturbation of the CD4+ and CD8+ T-cell subsets following infection with ***human*** ***immunodeficiency*** ***virus*** (***HIV***) is selective based on ***TCR*** variable (V) region gene expression. To address this question, we have functionally analyzed ***TCR*** V gene expression on CD8+ cytotoxic T lymphocytes from ***HIV*** -1-infected individuals. This was done using monoclonal ***antibodies*** against individual ***TCR*** V regions to trigger redirected cytolysis in 51Cr release assays. The percent specific lysis induced by each ***antibody*** functionally measures the representation of the ***TCR*** V region gene product it is specific for. Relative to non- ***HIV*** -infected controls and asymptomatic ***HIV*** -infected individuals with only moderate CD4 lymphocyte depletion, ***HIV*** -infected individuals with low CD4 lymphocyte counts exhibited skewed patterns of ***TCR*** V region representation. Therefore, the perturbation within the CD8+ cytotoxic T lymphocyte repertoire in ***HIV*** infection appears to be selective based on ***TCR*** V region usage, increasingly so as disease progresses. The ***TCR*** V genes affected varied between different ***HIV*** -infected individuals and skewing detected in functional assays was not always apparent by flow cytometric analysis. These results suggest that ***HIV*** infection causes generalized effects on the T-cell repertoire, which are reflected in the relative ***TCR*** V gene representation of the CD8+ cytotoxic T lymphocyte population in peripheral blood.

L4 ANSWER 13 OF 20 MEDLINE
95062162 Document Number: 95062162. PubMed ID: 7971973.
Autoantibodies to the alpha/beta T-cell receptors in ***human*** ***immunodeficiency*** ***virus*** infection: ***dysregulation*** and mimicry. Lake D F; Schluter S F; Wang E; Bernstein R M; Edmundson A B; Marchalonis J J. (College of Medicine, University of Arizona, Tucson 85724.) PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1994 Nov 8) 91 (23) 10849-53. Journal code: PV3; 7505876. ISSN: 0027-8424. Pub. country: United States. Language: English.

AB Autoimmune reactivity is a consequence of infection with ***human*** ***immunodeficiency*** ***virus*** (***HIV***). We studied serological cross-reactions of purified pooled IgG from sera of ***HIV*** -infected individuals by using nested sets of synthetic overlapping peptides duplicating the covalent structures of T-cell receptors (TCRs) and immunoglobulin light chains and report that two processes of ***autoantibody*** production occur. (i) IgG ***autoantibodies*** to putative regulatory variable domain CDR1 and FR3 epitopes (where CDR is complementarity-determining region and FR is framework region) are present in pooled IgG from ***HIV*** -infected individuals at levels 10-fold greater than that in pooled IgG from healthy humans. (ii) Anti- ***TCR*** autoimmunization involves antigenic mimicry between a conserved peptide stretch of the major neutralizing V3 loop determinant of ***HIV*** -1 gp120 and the conserved FR4 segment of the ***TCR*** V beta. Affinity-purified ***antibodies*** to the synthetic V3 loop peptide bound to a recombinant single-chain ***TCR*** and to a synthetic ***TCR*** joining segment peptide containing the FR4 sequence. Conversely, affinity-purified ***autoantibodies*** from pooled IgG from ***HIV*** -infected individuals to the ***TCR*** peptide bound the V3 loop peptide and a single-chain ***TCR*** . Inhibition studies indicated that the cross-reactive immunizing antigen was the V3 loop. These results bear upon the impact of ***HIV*** infection on immune regulation and on the selection of peptides for vaccine development.

L4 ANSWER 10 OF 20 MEDLINE
95285607 Document Number: 95285607. PubMed ID: 7768037. Autoreactivity in ***HIV*** -1 infection: the role of molecular mimicry. Silvestris F; Williams R C Jr; Dammacco F. (Department of Biomedical Sciences and Human Oncology, University of Bari, Italy.) CLINICAL IMMUNOLOGY AND IMMUNOPATHOLOGY, (1995 Jun) 75 (3) 197-205. Ref: 59. Journal code: DEA; 0356637. ISSN: 0090-1229. Pub. country: United States. Language: English.

AB Autoimmunity during ***HIV*** -1 infection may contribute to the ***immunopathogenesis*** of AIDS. Titers of ***autoantibodies*** to HLA molecules and other surface markers of CD4+ T cells appear to increase with the progression of disease and may correlate with lymphopenia. Other ***autoantibodies*** are directed at a number of regulatory molecules of the immune system. Genesis of autoreactivity may be related to structural homologies of ***HIV*** -1 env-products to such functional molecules involved in the control of self-tolerance. The most impressive similarities include the HLA-DR4 and DR2, the variable regions of ***TCR*** alpha-, beta-, and gamma-chain, the Fas protein, and several functional domains of IgG and IgA. Thus, ***HIV*** -1 infection may induce ***dysregulation*** leading to autoimmune response, through a number of molecular mimicry mechanisms. Pathogenicity of ***antibodies*** to T cells could also include the activation of membrane-to-nucleus signal transducers resulting in increased apoptosis. The evolution of autoimmune mechanisms during ***HIV*** -1 infection cannot exclude, however, progression to immunoproliferative malignancy, since aspects of oligoclonal immune response to ***HIV*** -1 components may occur in several autoimmune diseases which in some instances evolve to lymphoma.

L4 ANSWER 1 OF 20 MEDLINE
2001495648 Document Number: 21429276. PubMed ID: 11544282. ***HIV*** -1 infection impairs cell cycle progression of CD4(+) T cells without affecting early activation responses. Sieg S F; Harding C V; Lederman M M. (Department of Medicine, Division of Infectious Diseases, Center for AIDS Research, Case Western Reserve University, Cleveland, Ohio, USA.) JOURNAL OF CLINICAL INVESTIGATION, (2001 Sep) 108 (5) 757-64. Journal code: HS7; 7802877. ISSN: 0021-9738. Pub. country: United States. Language: English.

AB Failure of CD4(+) T cells to proliferate in response to antigenic stimulation is a characteristic of ***HIV*** infection. Analysis of the proliferation defect has been hampered by an inability to identify CD4(+) cells with ***T*** ***cell*** ***receptor*** specificity for antigen. To focus only on cells that had been stimulated through the ***T*** ***cell*** ***receptor*** , CD4(+) T cells were stimulated with an anti-Vbeta3 Ab that activates approximately 3-5% of peripheral blood T cells. This approach revealed proliferation defects in cells from ***HIV*** -infected patients that were not appreciated using anti-CD3 Ab stimulation and provided the capacity to examine responses on a single cell basis. After anti-Vbeta3 Ab stimulation, CD4(+)Vbeta3(+) cells from ***HIV*** -infected patients demonstrated defects in expression of cell cycle-associated proteins, D-type cyclins, and cyclin A. However, the expression of early activation markers, CD69 and CD25, was not significantly impaired in cells from most patients. Thus, CD4(+) T cell proliferation failure in ***HIV*** disease is characterized by dysregulated activation that precludes cell cycle progression. This proliferation defect was most apparent in patients with diminished CD4(+) T cell numbers and higher plasma ***HIV*** RNA levels. CD4(+) T cell proliferation failure may be a key determinant of immune ***impairment*** in ***HIV*** disease.

L6 ANSWER 7 OF 9 MEDLINE

95207724 Document Number: 95207724. PubMed ID: 7899820. The ***T*** ***cell*** ***receptor*** and AIDS pathogenesis. Hoffmann G W. (Department of Microbiology and Immunology, University of British Columbia, Vancouver, Canada.) SCANDINAVIAN JOURNAL OF IMMUNOLOGY, (1995 Apr) 41 (4) 331-7. Journal code: UCW; 0323767. ISSN: 0300-9475. Pub. country: ENGLAND: United Kingdom. Language: English.

AB An idiotypic network model of AIDS pathogenesis is described in which the ***T*** ***cell*** ***receptor*** plays a role both in infection and as a target of autoimmunity. This is an extension of a previously published autoimmunity model, and provides explanations for several otherwise puzzling aspects of AIDS pathogenesis. In the model ***HIV*** -specific T cells are preferentially infected, and ***HIV*** , acting as an antigen, stimulates the expansion of the infectable pool of T cells. The ***HIV*** variants that are most strongly selected are those that are recognized by the most helper T cells. ***HIV*** and suppressor T cells are subject to the same selective environment, and consequently undergo a process of convergent selection to resemble each other more and more with time. Eventually immunity against ***HIV*** cross-reacts with suppressor T cell idiotypes, disrupting the normal regulation of helper T cells. Autoimmunity ensues. The model leads to novel vaccine and therapy approaches involving the targeting and elimination of ***HIV*** -specific T cells.

L6 ANSWER 2 OF 9 MEDLINE
97153482 Document Number: 97153482. PubMed ID: 9000486. Analysis of ***autoantibodies*** to T-cell receptors among ***HIV*** -infected individuals: epitope analysis and time course. Marchalonis J J; Ampel N M; Schluter S F; Garza A; Lake D F; Galgiani J N; Landsperger W J. (College of Medicine, University of Arizona, Tucson, Arizona, 85724, USA.) CLINICAL IMMUNOLOGY AND IMMUNOPATHOLOGY, (1997 Feb) 82 (2) 174-89. Journal code: DEA; 0356637. ISSN: 0090-1229. Pub. country: United States. Language: English.

AB Individuals seropositive for ***human*** ***immunodeficiency*** ***virus*** type 1 (***HIV***) express elevated levels of ***autoantibodies*** (AAbs) directed against recombinant T-cell receptors (TCRs) and synthetic peptide epitopes duplicating beta chain markers. We performed longitudinal studies of anti- ***TCR*** AAbs in ***HIV*** -1-infected individuals, making comparisons with uninfected sera and sera from other individuals infected with a nonviral agent. We determined levels of ***autoantibodies*** by titration using enzyme-linked immunosorbent assay (ELISA) and developed a means for characterizing " ***autoantibody*** CDR recognition spectrotypes" for individual sera. Antibody levels against certain defined synthetic epitopes were substantially elevated in ***HIV*** -infected subjects relative to reactivities by control groups. Individual sera showed relatively high AAb levels to a subset of CDR1 peptide epitopes. Two patients who subsequently developed AIDS showed particular reactivity to Vbeta2.1, 8.1, 10.1, and 22.1 epitopes. Our results show that production AAbs to ***TCR*** Vbeta epitopes is a general consequence of ***HIV*** infection. The response is individual but shows some restriction and shifts in AAb subpopulations often occur with time.

L15 ANSWER 2 OF 19 MEDLINE
2001197651 Document Number: 21151071. PubMed ID: 11256574. Emerging principles for ***T*** ***cell*** ***receptor*** recognition of antigen in cellular immunity. Garcia K C; Degano M; Speir J A; Wilson I A. (The Scripps Research Institute, Department of Molecular Biology, La Jolla, CA 92037, USA.) Rev Immunogenet, (1999) 1 (1) 75-90. Ref: 75. Journal code: D09; 100883703. ISSN: 1398-1714. Pub. country: Sweden.

Language: English.

AB The structural basis of antigen recognition in cellular immunity has been elucidated through the determination of crystal structures of major histocompatibility complex (MHC) molecules bound to antigenic peptides, T cell receptors (***TCR***), CD8 and CD4 co-receptors and, most recently, TCRs in complex with peptide-MHC (pMHC). The mechanisms that generate the diversity of the immune response to invading microorganisms were first realized at a genetic level and are necessary in order to cope with the enormous number of potential antigens. This diversity is manifested in the protein products of the genes which code for the components of the ***TCR*** signalling complex. The structure of the ***TCR*** reveals both striking similarities with and fundamental differences from its ***functional*** counterpart, the antibody, in the humoral immune system. The conserved manner in which the ***TCR*** recognizes and interacts with its peptide-MHC ligand allows the ***TCR*** great latitude in its potential to form productive interactions with antigen-presenting cells that bear numerous ligands to which the ***TCR*** has not been previously exposed. This phenomenon of cross-, or alloreactivity arises from a combination of conserved structural features across all MHC molecules, both self and foreign, and some degree of molecular mimicry. Non-classical MHC ligands presenting either modified or specialized peptides, lipids, carbohydrates, or no ligand at all, are now thought to play increasingly important roles in cellular immunity. We ***review*** some of the recent structural results and our current state of knowledge about ***TCR*** structure, and how this relates to its ***function*** .

L15 ANSWER 10 OF 19 MEDLINE
97077676 Document Number: 97077676. PubMed ID: 8920243. Variant ***TCR*** ligands: new insights into the molecular basis of antigen-dependent signal transduction and T-cell activation. Madrenas J; Germain R N. (Laboratory of Immunology, National Institute of Allergy and Infectious Diseases, Bethesda, MD 20892-1892, USA.) SEMINARS IN IMMUNOLOGY, (1996 Apr) 8 (2) 83-101. Ref: 99. Journal code: A61; 9009458. ISSN: 1044-5323. Pub. country: United States. Language: English.

AB Recent studies have identified peptide-MHC molecule ligands of alpha beta T-cell receptors with properties apparently distinct from classical agonists. These complexes, which are slight structural variants of the immunizing peptide or original presenting MHC molecule, have several novel properties. They can act as partial agonists able to induce only some and not other effector activities of the T cell, as antagonists able to inhibit T-cell ***functions*** stimulated by agonist ligand, or as mixed partial agonists/antagonists. Here we discuss the existing data suggesting that a simple receptor occupancy model does not account for the properties of these ***TCR*** ligands and ***review*** emerging data on qualitative differences in signal transduction following ***TCR*** engagement by priming versus variant complexes. We propose several non-exclusive models to explain both the biochemical and biological properties of variant ligands with partial agonist or antagonist properties.

L15 ANSWER 11 OF 19 MEDLINE
96303221 Document Number: 96303221. PubMed ID: 8732480. ***TCR*** gene polymorphisms and autoimmune disease. Kay R A. (Department of Pathology, Ninewells Hospital & Medical School, Dundee, UK.) EUROPEAN JOURNAL OF IMMUNOGENETICS, (1996 Apr) 23 (2) 161-77. Ref: 129. Journal code: AZ6; 9106962. ISSN: 0960-7420. Pub. country: ENGLAND: United Kingdom. Language: English.

AB Autoimmunity may result from abnormal regulation within the immune system. As the T cell is the principal regulator of the immune system and its normal ***function*** depends on immune recognition or self/non-self discrimination, abnormalities of the idiotypic ***T*** - ***cell*** ***receptor*** (***TCR***) may be one cause of autoimmune disease. The ***TCR*** is a clonally distributed, cell-surface heterodimer which binds peptide antigen when complexed with HLA molecules. In order to recognize the variety of antigens it may possibly encounter, the ***TCR*** , by necessity, is a diverse structure. As with immunoglobulin, it is the variable domain of the ***TCR*** which interacts with antigen and exhibits the greatest amount of amino acid variability. The underlying genetic basis for this structural diversity is similar to that described for immunoglobulin, with ***TCR*** diversity relying on the somatic recombination, in a randomly imprecise manner, of smaller gene segments to form a ***functional*** gene. There are a large number of gene segments to choose from (particularly the TCRAV, TCRAJ and TCRBV gene segments) and some of these also exhibit allelic variation. Finally, polymorphisms in non-coding regions of ***TCR*** genes, leading to biased recombination or expression, are also beginning to be recognized. All these factors contribute to the polymorphic nature of the ***TCR*** , in terms of both structure and repertoire formation. It follows that inherited abnormalities in either coding or regulatory regions of ***TCR*** genes may predispose to aberrant T-cell ***function*** and autoimmune disease. This ***review*** will outline the genomic organization of the ***TCR*** genes, the genetic mechanisms responsible for the generation of diversity, and the results of investigations into the association between germline polymorphisms and autoimmune disease.

L15 ANSWER 15 OF 19 MEDLINE
94137363 Document Number: 94137363. PubMed ID: 8305133. Tickling the ***TCR*** : selective T-cell ***functions*** stimulated by altered peptide ligands. Evavold B D; Sloan-Lancaster J; Allen P M. (Dept of Pathology, Washington University School of Medicine, St Louis, MO 63110.) IMMUNOLOGY TODAY, (1993 Dec) 14 (12) 602-9. Ref: 60. Journal code: AEA; 8008346. ISSN: 0167-5699. Pub. country: ENGLAND: United Kingdom. Language: English.

AB Recent observations of T-cell responses following ***T*** - ***cell*** ***receptor*** (***TCR***) interaction with altered peptide ligands have highlighted the complexity of this signalling system. The indications are that the ***TCR*** responds to minor changes in ligand with gradations of T-cell activation and effector ***functions*** . Brian Evavold, Joanne Sloan-Lancaster and Paul Allen ***review*** these studies and present a model in which partial T-cell activation and ***TCR*** antagonism are related events in a continuum of signalling through the ***TCR*** .

L15 ANSWER 17 OF 19 MEDLINE
92273160 Document Number: 92273160. PubMed ID: 1591001. The human ***T*** ***cell*** ***receptor*** in health and disease. Moss P A; Rosenberg W M; Bell J I. (Institute of Molecular Medicine, John Radcliffe Hospital, Headington, Oxford, United Kingdom.) ANNUAL REVIEW OF IMMUNOLOGY, (1992) 10 71-96. Ref: 139. Journal code: ALO; 8309206. ISSN: 0732-0582. Pub. country: United States. Language: English.

AB The T cell antigen receptor (***TCR***) recognizes antigen in the form of short peptides bound to a major histocompatibility (MHC) molecule. This ***review*** provides a synopsis of the current state of knowledge of the structure and ***function*** of the receptor and its possible role in human disease. Analysis of the ***T*** ***cell***

receptor usage of T-cell lines and clones recognizing the same peptide-MHC complex is beginning to shed light onto the structural basis of the ***TCR*** -peptide-MHC complex. Also, it is now apparent that there are two mechanisms by which the ***TCR*** can interact with the MHC molecule, either through classical peptide interactions or through super-antigens. Finally, we ***review*** the role of specific TCRs in human disease. Current evidence in this area is difficult to interpret; however, it is likely that ***TCR*** -mediated disease susceptibility exists, and its basis at either a germline or somatic level will soon be clarified.

L24 ANSWER 1 OF 3 WPIDS COPYRIGHT 2002 DERWENT INFORMATION LTD
AN 1999-357172 [30] WPIDS
DNC C1999-105556
TI Delaying onset of AIDS in a host infected with an immunodeficiency-type retrovirus.
DC B04
IN DEHGHANPISHEH, K; HUANG, D S; ***MARCHALONIS, J J*** ; WANG, Y; WATSON, R R
PA (ARIZ-N) ARIZONA BOARD OF REGENTS
CYC 1
PI US 5911990 A 19990615 (199930)* 13p
ADT US 5911990 A US 1996-696049 19960813
PRAI US 1996-696049 19960813

AB US 5911990 A UPAB: 19990802
NOVELTY - Administration of a peptide (I) corresponding to the first complementarity determining region of T-cell receptor V beta (TCR V beta CDR1) to a host infected with an immunodeficiency type retrovirus results in the prevention of retrovirus-induced suppression of immune responses and normalizes cytokine production.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are included for:

(1) a method of modulating the immune response of a mammal infected with a C-type retrovirus or a lentivirus by administering (I) through a systemic route to stimulate production of T helper 1 (Th1) cytokines; interleukin 2 and interferon- gamma , and to suppress the production of T helper 2 (Th2); interleukins 5, 6 and 10 and immunoglobulin G; and

(2) a method of altering the immune system response of a host suffering from an infectious disease by artificially introducing (I) by injection into the host's bloodstream or immune system so that the immune system is artificially induced to stimulate production of Th1 cytokines or suppress production of Th2 derived cytokines.

ACTIVITY - Anti-HIV.

MECHANISM OF ACTION - Immunomodulating agent.

(I) reduces the imbalance of Th1 and Th2 cytokine production and contributes to the normalization of the immune response which retards development of immune dysfunction.

Female C57B1/6 5 week old mice were set up in 3 treatments: (1) LP-BM5 retrovirus infected mice injected with saline, (2) LP-BM5 retrovirus infected mice injected with control peptide MCG3, or (3) LP-BM5 retrovirus infected mice injected with TCR V beta CDR1. Administration of peptides (200 micro g/mice in saline, i.p.) was carried out twice on days 7 and 3 before retrovirus infection. Peptide preparations were free of endotoxins and for TCR V beta CDR1 comprised the sequence Cys Lys Pro Ile Ser Gly His Asn Ser Leu Phe Trp Tyr Arg Gln Thr corresponding to the human TCR V beta sequence and for the control sequence Thr Gly Thr Ser Ser Asp Val Gly Gly Tyr Asn Tyr Val Ser Trp Tyr corresponding to the CDR1 of the L chain MCG. The LP-BM5 retrovirus was administered i.p. to mice on 0.1 ml with an electrophic titer of 4.5 log10 PFU/ml which leads to rapid induction of clinical symptoms with virtually no latent phase.

After 42 days of retroviral infection immunological analysis was carried out. Specific titers of serum IgG to TCR- beta and MCG3 were determined by enzyme linked immunosorbent assay (ELISA). IgG production by LPS-stimulated splenocytes, an indication of early retrovirus infection during the progression to murine AIDS, was significantly reduced (p less than 0.05) by TCR V beta administration before infection but administration of control peptide MCG3 showed no effect.

Treatment of retrovirally infected mice with (I) did not result in a significant increase in mean Ab titers compared with either retrovirally infected saline treated mice or retrovirally infected control treated mice. In vitro production of Th1 cytokines, Il-2 and IFN- gamma by

concanavalin A-stimulated splenocytes was significantly (p less than 0.05) inhibited and normalized in the retrovirus infected mice administered with TCR V beta before infection but not in those administered the control peptide MCG3. Release of TNF- alpha by LPS-stimulated splenocytes was significantly inhibited in retrovirally infected mice administered with TCR V beta (p less than 0.05).

USE - Administration of (I) is used to delay the onset of AIDS through the restoration of normal levels of Th1 cytokines and Th2 derived cytokines and extends the period that occurs between infection by the retrovirus and the appearance of immune deficiencies. It causes the deleterious effects of infection to be reversed through prevention of immunosuppression and cytokine dysregulation that is otherwise induced by infection with an immunodeficiency-type retrovirus.

Studying (I) gives an insight into the pathogenesis occurring that leads to AIDS and into the idiotypic networks that involve autoantibodies and autoreactive T cells as regulatory elements and an understanding of the role of Vitamin E in immune function during retrovirus infection.

GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 9, 2002, 10:50:13 ; Search time 23.89 Seconds
(without alignments)
49.610 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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22: /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	96	100.0	16	20	AAY17984	Peptide derived fr
2	96	100.0	312	6	AAP50079	T-cell antigen rec
3	96	100.0	312	7	AAP60471	Portion of a human
4	82	85.4	312	15	AAR53145	T-cell antigen rec
5	80	83.3	114	13	AAR26960	Human T lymphocyte
6	74	77.1	79	13	AAR26969	Human T lymphocyte
7	74	77.1	92	15	AAR65454	T-cell receptor V-
8	74	77.1	93	20	AAY23521	Amino acid sequenc
9	74	77.1	94	16	AAR78686	T-cell receptor be
10	74	77.1	96	16	AAR78687	T-cell receptor be
11	74	77.1	104	15	AAR65453	T-cell receptor V-
12	74	77.1	106	20	AAY23520	Amino acid sequenc
13	74	77.1	113	15	AAR65450	T-cell receptor V-
14	74	77.1	113	15	AAR65455	T-cell receptor V-
15	74	77.1	114	20	AAY23517	Amino acid sequenc
16	74	77.1	114	20	AAY23522	Amino acid sequenc
17	74	77.1	311	21	AAY96291	Human IGFAM-3 immu
18	74	77.1	314	20	AAW99374	Human T-cell recep
19	73	76.0	113	15	AAR65452	T-cell receptor V-
20	73	76.0	114	13	AAR26968	Human T lymphocyte
21	73	76.0	114	20	AAY23519	Amino acid sequenc
22	72	75.0	113	15	AAR65451	T-cell receptor V-
23	72	75.0	114	20	AAY23518	Amino acid sequenc
24	72	75.0	314	20	AAY15229	Human receptor pro
25	70	72.9	79	13	AAR26964	Human T lymphocyte
26	70	72.9	114	15	AAR65467	T-cell receptor V-
27	70	72.9	114	20	AAY23534	Amino acid sequenc
28	70	72.9	137	18	AAW25939	T-cell receptor V-
29	70	72.9	287	21	AAY56079	Mouse H2-Dd/flu nu
30	70	72.9	287	21	AAY56081	HLA-A2/HIV gag res
31	70	72.9	287	21	AAY57855	TCR beta chain and
32	70	72.9	287	21	AAY57857	TCR beta chain and
33	69	71.9	113	15	AAR65456	T-cell receptor V-
34	69	71.9	114	20	AAY23523	Amino acid sequenc
35	68	70.8	312	21	AAY69988	Human receptor-ass
36	65	67.7	92	16	AAR79171	TCR Vbeta5.3. Hom
37	63	65.6	345	21	AAY69986	Human receptor-ass
38	62	64.6	112	21	AAY83752	Canine T-cell rece
39	62	64.6	112	21	AAY80667	Canine TCR V-beta
40	62	64.6	113	21	AAY83753	Canine T-cell rece
41	62	64.6	113	21	AAY80668	Canine TCR V-beta
42	62	64.6	114	21	AAY80585	Canine T-cell rece
43	62	64.6	114	21	AAY83754	Canine T-cell rece
44	62	64.6	114	21	AAY80650	Canine TCR V-beta
45	62	64.6	114	21	AAY80669	Canine TCR V-beta

ALIGNMENTS

RESULT 1
AAY17984
ID AAY17984 standard; peptide; 16 AA.
XX
AC AAY17984;
XX
DT 09-AUG-1999 (first entry)
XX
DE Peptide derived from human T-cell receptor Vbeta gene product.
XX
KW T-cell receptor; TCR; immunodeficiency type retrovirus; immune response;
KW cytokine; C-type retrovirus; lentivirus; T helper 1; Th1; interleukin;
KW interferon-gamma; Th2; immunoglobulin G; AIDS; immune deficiency;
KW immunosuppression; cytokine dysregulation; TCR Vbeta gene.
XX
OS Homo sapiens.
XX
PN US5911990-A.
XX
PD 15-JUN-1999.
XX
PF 13-AUG-1996; 96US-0696049.
XX
PR 13-AUG-1996; 96US-0696049.
XX
PA (ARIZ-) ARIZONA BOARD OF REGENTS.
XX
PI Dehghanpisheh K, Huang DS, Marchalonis JJ, Wang Y;
PI Watson RR;
XX
DR WPI; 1999-357172/30.
XX
PT Delaying onset of AIDS in a host infected with an
PT immunodeficiency-type retrovirus

```
XX
PS   Claim 3; Column 9; 13pp; English.
XX
CC   The invention relates to a peptide (I) corresponding to the first
CC   complementarity determining region of T-cell receptor V beta (TCR V beta
CC   Administering this peptide to a host infected with an immunodeficiency
CC   type retrovirus results in the prevention of retrovirus-induced
CC   suppression of immune responses and normalizes cytokine production. The
CC   invention describes(1) a method of modulating the immune response of a
CC   mammal infected with a C-type retrovirus or a lentivirus by administering
CC   the TCR peptide through a systemic route to stimulate production of T
CC   helper 1 (Th1) cytokines; interleukin 2 and interferon-gamma, and to
CC   suppress the production of T helper 2 (Th2); interleukins 5, 6 and 10 and
CC   immunoglobulin G; and (2) a method of altering the immune system response
CC   of a host suffering from an infectious disease by artificially
CC   introducing the peptide by injection into the host's bloodstream or
CC   immune system so that the immune system is artificially induced to
CC   stimulate production of Th1 cytokines or suppress production of Th2
CC   derived cytokines. Administration of the peptide is used to delay the
CC   onset of AIDS through the restoration of normal levels of Th1 cytokines
CC   and Th2 derived cytokines and extends the period that occurs between
CC   infection by the retrovirus and the appearance of immune deficiencies. It
CC   causes the deleterious effects of infection to be reversed through
CC   prevention of immunosuppression and cytokine dysregulation that is
CC   otherwise induced by infection with an immunodeficiency-type retrovirus.
CC   The present sequence represents the peptide of the invention derived from
CC   TCR Vbeta gene product.
XX
SQ   Sequence   16 AA;


  Query Match             100.0%;  Score 96;  DB 20;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 5.9e-09;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          ||||||||||||||||
Db      1 ckpisghnslfwyrqt 16


RESULT   2
AAP50079
ID   AAP50079 standard; protein; 312 AA.
XX
AC   AAP50079;
XX
DT   19-MAR-1992  (first entry)
XX
DE   T-cell antigen receptor protein.
XX
KW   T-cell receptor; DNA probe; tumor marker; ss.
XX
PN   EP149548-A.
XX
PD   24-JUL-1985.
XX
PF   14-JAN-1985;   85EP-0300243.
XX
PR   06-FEB-1984;   84US-0577526.
XX
PA   (ONTA-) ONTARIO CANCER INST.
XX
PI   Mak TW;
XX
DR   WPI; 1985-179193/30.
DR   N-PSDB; AAN50091.
XX
PT   New nucleic acid encoding T-cell antigen receptor polypeptide -
PT   useful for prepn.. of probes or antibodies for detection of
PT   tumour cells and T-cells
XX
PS   Disclosure; Fig 3; 15pp; English.
XX
CC   This protein resembles human and mouse Ig light chain
CC   molecules.  This protein is encoded by clone YT35 and is
CC   part of the antigen receptor mediating specialized T-
CC   lymphocyte function. Antibodies may be directed against
CC   this protein and used for detection of T-cell receptor
CC   antigen so that unknown cells, e.g. a tumor cell, can be
CC   identified as a T-cell or other cell.
XX
SQ   Sequence   312 AA;


  Query Match             100.0%;  Score 96;  DB 6;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          ||||||||||||||||
Db     42 ckpisghnslfwyrqt 57


RESULT   3
AAP60471
ID   AAP60471 standard; Protein; 312 AA.
XX
AC   AAP60471;
XX
DT   13-JUN-1991  (first entry)
XX
DE   Portion of a human T-cell antigen receptor protein.
XX
KW   Cancer; tumour cell; T-cell receptor.
XX
OS   Homo sapiens.
XX
PN   CA1197480-A.
XX
PD   03-DEC-1985.
XX
PF   01-FEB-1984;   84CA-0446545.
XX
PR   01-FEB-1984;   84CA-0446545.
XX
PA   (ONTA-) ONTARIO CANCER INST.
XX
PI   Mak TW;
XX
DR   WPI; 1986-007147/02.
DR   N-PSDB; AAN60406.
XX
PT   New pure nucleic acid with sequence encoding T-cell polypeptide -
PT   is prepd. by recombinant DNA methods for use as probe when
PT   labelled and for antibody prodn.
XX
PS   Claim 4; Fig 3; 22pp; English.
XX
CC   Receptor protein product has at least 60% homology with the clone YT
CC   35. The product resembles human and mouse Ig light chain molecules,
CC   and may be labelled for use as a probe for the detection of the
CC   T-cell receptor antigen, and identification of unknown (esp. tumour
CC   cells) as T-cells.
XX
SQ   Sequence   312 AA;


  Query Match             100.0%;  Score 96;  DB 7;  Length 312;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-07;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          ||||||||||||||||
Db     42 ckpisghnslfwyrqt 57
```

```
RESULT   4
AAR53145
ID   AAR53145 standard; Protein; 312 AA.
XX
AC   AAR53145;
XX
DT   08-SEP-1994  (first entry)
XX
DE   T-cell antigen receptor.
XX
KW   T-cell antigen receptor; T-lymphocyte; probe; hybridization; MOLT-3.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 90
FT                   /note= "possible N-glycosylation site"
FT   Misc-difference 205
FT                   /note= "possible N-glycosylation site"
XX
PN   EP593092-A.
XX
PD   20-APR-1994.
XX
PF   14-JAN-1985;   85EP-0118895.
XX
PR   13-JAN-1984;   84US-0570694.
PR   06-FEB-1984;   84US-0577526.
XX
PA   (ONTA-) ONTARIO CANCER INST.
XX
PI   Mak TW;
XX
DR   WPI; 1994-127936/16.
DR   N-PSDB; AAQ62128.
XX
PT   New nucleic acid encoding T-cell antigen receptor - is useful
PT   e.g. as a probe to identify T-cells
XX
PS   Disclosure; Fig 3; 13pp; English.
XX
CC   mRNA complementary to the DNA sequence given in AAQ62128 is obtained by
CC   isolating mRNA from MOLT-3 cells, preparing cDNA, inserting the cDNA
CC   into the BglII site of vector pFP502EB5, transfecting the vector into
CC   Escherichia coli HB101, and screening for 1.3 kb T-cell specific
CC   mRNA in MOLT-3 and HSC-58 cells.  The mRNA encodes a portion of the
CC   T-cell antigen receptor (sequence AAR53145).
XX
SQ   Sequence   312 AA;


  Query Match             85.4%;  Score 82;  DB 15;  Length 312;
  Best Local Similarity   93.8%;  Pred. No. 2.3e-05;
  Matches   15;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          ||||||||||| ||||
Db     42 ckpisghnslfsyrqt 57


RESULT   5
AAR26960
ID   AAR26960 standard; Protein; 114 AA.
XX
AC   AAR26960;
XX
DT   11-FEB-1993  (first entry)
XX
DE   Human T lymphocyte receptor V-beta w21 subfamily segment.
XX
KW   TCR; IGR b 02; variable region; immunomodulation;
KW   polymerase chain reaction; T cell receptor.
XX
OS   Homo sapiens.
XX
PN   WO9213950-A.
XX
PD   20-AUG-1992.
XX
PF   12-FEB-1992;   92WO-FR00130.
XX
PR   12-FEB-1991;   91FR-0001613.
PR   12-APR-1991;   91FR-0004523.
XX
PA   (ROUS ) ROUSSEL-UCLAF.
XX
PI   Ferradini L,  Hercend T,  Roman-Roman S,  Triebel F;
XX
DR   WPI; 1992-300036/36.
DR   N-PSDB; AAQ28173.
XX
PT   Variable regions of b-chain of T-lymphocyte receptors and their
PT   DNA - useful as immuno:modulant(s) and for diagnosing immune
PT   disorders
XX
PS   Claim 7; Page 37; 75pp; French.
XX
CC   RNA was isolated from peripheral lymphocytes and converted to cDNA
CC   using a C-beta-specific primer. The cDNA was amplified by anchored
CC   PCR using C-beta and polyC primers, then amplified again using a
CC   different C-beta specific primer. The amplified product was SacII-
CC   restricted, inserted into Bluescript SK+ vector and used to transform
CC   E.coli XL-1blue. Transformants were screened with a C-beta specific
CC   probe and DNA from positive clones was sequenced in the C-beta
CC   region. The sequence designated "IGR b 02" has ca. 85% homology
CC   with the sequence HSTCRB23 (see Wilson R.K. et al., Immunogenetics
CC   32:406, 1990) and is a member of the Vbeta w21 subfamily. The
CC   peptide encoded by it can be used to block T cell epitopes and in
CC   vaccines. See also AAQ28174-Q28228.
XX
SQ   Sequence   114 AA;


  Query Match             83.3%;  Score 80;  DB 13;  Length 114;
  Best Local Similarity   80.0%;  Pred. No. 1.7e-05;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQ 15
          | |||||||:|:|||| 
Db     42 cnpisghntlywyrq 56


RESULT   6
AAR26969
ID   AAR26969 standard; Protein; 79 AA.
XX
AC   AAR26969;
XX
DT   11-FEB-1993  (first entry)
XX
DE   Human T lymphocyte receptor V-beta 6 subfamily segment.
XX
KW   TCR; IGR b 12; variable region; immunomodulation;
KW   polymerase chain reaction; T cell receptor.
XX
OS   Homo sapiens.
XX
PN   WO9213950-A.
XX
PD   20-AUG-1992.
XX
PF   12-FEB-1992;   92WO-FR00130.
XX
PR   12-FEB-1991;   91FR-0001613.
PR   12-APR-1991;   91FR-0004523.
XX
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PA (ROUS) ROUSSEL-UCLAF.
XX
PI Ferradini L, Hercend T, Roman-Roman S, Triebel F;
XX
DR WPI; 1992-300036/36.
DR N-PSDB; AAQ28182.
XX
PT Variable regions of b-chain of T-lymphocyte receptors and their
PT DNA - useful as immuno:modulant(s) and for diagnosing immune
PT disorders
XX
PS Claim 7; Page 46; 75pp; French.
XX
CC RNA was isolated from peripheral lymphocytes and converted to cDNA
CC using a C-beta-specific primer. The cDNA was amplified by anchored
CC PCR using C-beta and polyC primers, then amplified again using a
CC different C-beta specific primer. The amplified product was SacII-
CC restricted, inserted into Bluescript SK+ vector and used to transform
CC E.coli XL-1blue. Transformants were screened with a C-beta specific
CC probe and DNA from positive clones was sequenced in the C-beta
CC region. The sequence designated "IGR b 12" represents a new member
CC of the V beta 6 subfamily and has a homology of 94% with three
CC previously identified members of the V beta 6 subfamily. The peptide
CC encoded by it can be used to block T cell epitopes and in vaccines.
CC See also AAQ28173-Q28228.
XX
SQ Sequence 79 AA;

Query Match 77.1%; Score 74; DB 13; Length 79;
Best Local Similarity 68.8%; Pred. No. 0.00011;
Matches 11; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CKPISGHNSLFWYRQT 16
| ||||| :|:||||:
Db 7 cdpisghtalywyrqs 22

RESULT 7
AAR65454
ID AAR65454 standard; protein; 92 AA.
XX
AC AAR65454;
XX
DT 24-MAY-1995 (first entry)
XX
DE T-cell receptor V-beta HUVB6.9.
XX
KW T-cell receptor; TCR; T-lymphocyte receptor; variable region;
KW beta-chain; V-beta; multiple sclerosis; cerebrospinal fluid;
KW autoimmune disease; lymphoma; vaccine.
XX
OS Homo sapiens.
XX
PN WO9425063-A.
XX
PD 10-NOV-1994.
XX
PF 29-APR-1994; 94WO-US04789.
XX
PR 29-APR-1993; 93US-0055006.
XX
PA (IMMU-) IMMUNE RESPONSE CORP.
PA (SAND-) SAN DIEGO REGIONAL CANCER CENT.
XX
PI Brostoff SW, Carlo DJ, Gold DP, Smith LR, Wilson DB;
XX
DR WPI; 1994-357913/44.
XX
PT New vaccine against multiple sclerosis using T-cell receptors
PT or fragments of T-cell receptors from the beta chain variable
PT region; for treating auto:immune disease and lymphoma(s)
XX
PS Disclosure; Fig. 2A; 43pp; English.
XX
CC Sequences of the T-cell receptor beta-chain variable region that
CC were most frequently expressed in cultures from the cerebrospinal
CC fluid of multiple sclerosis patients are given in AAR65450-67. A
CC peptide based on AAR65450-57 has been used for vaccine development.
XX
SQ Sequence 92 AA;

Query Match 77.1%; Score 74; DB 15; Length 92;
Best Local Similarity 75.0%; Pred. No. 0.00012;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CKPISGHNSLFWYRQT 16
| ||| || |:|||||
Db 21 cdpisehnrlywyrqt 36

RESULT 8
AAY23521
ID AAY23521 standard; Protein; 93 AA.
XX
AC AAY23521;
XX
DT 02-SEP-1999 (first entry)
XX
DE Amino acid sequence of human V beta 6.9.
XX
KW Vaccine; T cell receptor; TCR; T cell; V beta 6.2/3; V beta 6/5;
KW V beta 6.7; V beta 2; V beta 5/1; V beta 7; V beta 13; V beta 6;
KW multiple sclerosis.
XX
OS Homo sapiens.
XX
PN WO9927957-A1.
XX
PD 10-JUN-1999.
XX
PF 03-DEC-1997; 97WO-US23147.
XX
PR 03-DEC-1997; 97WO-US23147.
XX
PA (IMMU-) IMMUNE RESPONSE CORP.
PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI Brostoff SW, Carlo DJ, Gold DP, Smith LR, Wilson DB;
XX
DR WPI; 1999-404801/34.
XX
PT T0 cell receptor peptide-derived vaccines
XX
PS Example 8; Fig 2A-B; 104pp; English.
XX
CC The specification describes vaccines which comprise immunologically
CC effective amounts of T cell receptor (TCR) peptides. The TCRs are
CC present on the surface of T cells. The TCRs are chosen from V beta
CC 6.2/3, V beta 6/5, V beta 6.7, V beta 2, V beta 5/1, V beta 7 or V beta
CC 13. The V beta TCR peptide-based vaccines are useful for prevention or
CC treatment of multiple sclerosis (MS). The presence of V beta 6.7 appears
CC to be particularly associated with multiple sclerosis and can be used
CC to determine an individual's susceptibility to multiple sclerosis.
CC Vaccinating, rather than passively administering heterologous
CC antibodies, allows the host's own immune system to mobilize and suppress
CC auto aggressive T cells. Therefore, the suppression is persistent and
CC may involve any and all immunological mechanisms in effecting that
CC suppression. Such a multi-faceted response is more effective than
CC the uni-dimensional suppression achieved by passive administration of
CC monoclonal antibodies or extant-derived regulatory T cell clones.
CC AAY23517-34 represent human V beta proteins that are most frequently
CC expressed in the cerebrospinal fluid (CFS) of MS patients.
XX
SQ Sequence 93 AA;

```
  Query Match             77.1%;  Score 74;  DB 20;  Length 93;
  Best Local Similarity   75.0%;  Pred. No. 0.00013;
  Matches   12;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          | ||| || |:|||||
Db     21 cdpisehnrlywyrqt 36


RESULT   9
AAR78686
ID   AAR78686 standard; Protein; 94 AA.
XX
AC   AAR78686;
XX
DT   12-APR-1996  (first entry)
XX
DE   T-cell receptor beta-chain variable region V-beta-6.1.
XX
KW   Diabetes; immunotherapy; T-cell receptor beta-chain.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          46..59
FT                   /label= CDR2
FT                   /note= "Claim 7, page 27"
XX
PN   WO9521623-A1.
XX
PD   17-AUG-1995.
XX
PF   10-FEB-1995;   95WO-US01572.
XX
PR   14-FEB-1994;   94US-0195963.
XX
PA   (UYVE-) UNIV VERMONT.
XX
PI   Albertini RJ,  Falta MT;
XX
DR   WPI; 1995-292941/38.
DR   N-PSDB; AAQ96132.
XX
PT   Preventing or reducing severity of diabetes - by inhibiting the
PT   activity of specific T-cells, partic. by interfering with
PT   diabetes-associated T cell receptors
XX
PS   Claim 4; Fig 1; 42pp; English.
XX
CC   Non-conserved regions of T-cell receptor (TCR) beta-chain variable
CC   regions V-beta-6.1, V-beta-6.6/6.7 and V-beta-14 (AAR78686-88) are
CC   used in the prevention or therapy of diabetes.  Diabetes is
CC   characterised by predominant usage of TCRs bearing V-beta-6 and
CC   V-beta-14.  Such TCRs can be administered to a patient to generate
CC   an immune reaction that neutralises or kills V-beta-bearing T-cells.
CC   Hypervariable CDR2 regions (see AAR75364, AAR78689-90) of the V-beta-6
CC   and V-beta-14 chains may also be used.
XX
SQ   Sequence   94 AA;


  Query Match             77.1%;  Score 74;  DB 16;  Length 94;
  Best Local Similarity   68.8%;  Pred. No. 0.00013;
  Matches   11;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          | ||||| :|:||||:
Db     23 cdpisghtalywyrqs 38


RESULT  10
AAR78687
ID   AAR78687 standard; Protein; 96 AA.
XX
AC   AAR78687;
XX
DT   12-APR-1996  (first entry)
XX
DE   T-cell receptor beta-chain variable region V-beta-6.6./6.7.
XX
KW   Diabetes; immunotherapy; T-cell receptor beta-chain.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          48..61
FT                   /label= CDR2
FT                   /note= "Claim 8, page 28"
XX
PN   WO9521623-A1.
XX
PD   17-AUG-1995.
XX
PF   10-FEB-1995;   95WO-US01572.
XX
PR   14-FEB-1994;   94US-0195963.
XX
PA   (UYVE-) UNIV VERMONT.
XX
PI   Albertini RJ,  Falta MT;
XX
DR   WPI; 1995-292941/38.
DR   N-PSDB; AAQ96133.
XX
PT   Preventing or reducing severity of diabetes - by inhibiting the
PT   activity of specific T-cells, partic. by interfering with
PT   diabetes-associated T cell receptors
XX
PS   Claim 4; Fig 1; 42pp; English.
XX
CC   Non-conserved regions of T-cell receptor (TCR) beta-chain variable
CC   regions V-beta-6.1, V-beta-6.6/6.7 and V-beta-14 (AAR78686-88) are
CC   used in the prevention or therapy of diabetes.  Diabetes is
CC   characterised by predominant usage of TCRs bearing V-beta-6 and
CC   V-beta-14.  Such TCRs can be administered to a patient to generate
CC   an immune reaction that neutralises or kills V-beta-bearing T-cells.
CC   Hypervariable CDR2 regions (see AAR75364, AAR78689-90) of the V-beta-6
CC   and V-beta-14 chains may also be used.
XX
SQ   Sequence   96 AA;


  Query Match             77.1%;  Score 74;  DB 16;  Length 96;
  Best Local Similarity   68.8%;  Pred. No. 0.00013;
  Matches   11;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          | ||||| :|:||||:
Db     24 cdpisghtalywyrqs 39


RESULT  11
AAR65453
ID   AAR65453 standard; protein; 104 AA.
XX
AC   AAR65453;
XX
DT   24-MAY-1995  (first entry)
XX
DE   T-cell receptor V-beta HUVB6.5.
XX
KW   T-cell receptor; TCR; T-lymphocyte receptor; variable region;
KW   beta-chain; V-beta; multiple sclerosis; cerebrospinal fluid;
KW   autoimmune disease; lymphoma; vaccine.
```

```
XX
OS   Homo sapiens.
XX
PN   WO9425063-A.
XX
PD   10-NOV-1994.
XX
PF   29-APR-1994;   94WO-US04789.
XX
PR   29-APR-1993;   93US-0055006.
XX
PA   (IMMU-) IMMUNE RESPONSE CORP.
PA   (SAND-) SAN DIEGO REGIONAL CANCER CENT.
XX
PI   Brostoff SW,  Carlo DJ,  Gold DP,  Smith LR,  Wilson DB;
XX
DR   WPI; 1994-357913/44.
XX
PT   New vaccine against multiple sclerosis using T-cell receptors -
PT   or fragments of T-cell receptors from the beta chain variable
PT   region; for treating auto:immune disease and lymphoma(s)
XX
PS   Disclosure; Fig. 2A; 43pp; English.
XX
CC   Sequences of the T-cell receptor beta-chain variable region that
CC   were most frequently expressed in cultures from the cerebrospinal
CC   fluid of multiple sclerosis patients are given in AAR65450-67.  A
CC   peptide based on AAR65450-57 has been used for vaccine development.
XX
SQ   Sequence   104 AA;


  Query Match             77.1%;  Score 74;  DB 15;  Length 104;
  Best Local Similarity   75.0%;  Pred. No. 0.00014;
  Matches   12;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          | ||| || |:||||
Db     33 cdpisehnrlywyrqt 48


RESULT  12
AAY23520
ID   AAY23520 standard; Protein; 106 AA.
XX
AC   AAY23520;
XX
DT   02-SEP-1999  (first entry)
 X
DE   Amino acid sequence of human V beta 6.5.
XX
KW   Vaccine; T cell receptor; TCR; T cell; V beta 6.2/3; V beta 6/5;
KW   V beta 6.7; V beta 2; V beta 5/1; V beta 7; V beta 13; V beta 6;
KW   multiple sclerosis.
XX
OS   Homo sapiens.
XX
PN   WO9927957-A1.
XX
PD   10-JUN-1999.
XX
PF   03-DEC-1997;   97WO-US23147.
XX
PR   03-DEC-1997;   97WO-US23147.
XX
PA   (IMMU-) IMMUNE RESPONSE CORP.
PA   (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI   Brostoff SW,  Carlo DJ,  Gold DP,  Smith LR,  Wilson DB;
XX
DR   WPI; 1999-404801/34.
XX
PT   T0 cell receptor peptide-derived vaccines
XX
PS   Example 8; Fig 2A-B; 104pp; English.
XX
CC   The specification describes vaccines which comprise immunologically
CC   effective amounts of T cell receptor (TCR) peptides. The TCRs are
CC   present on the surface of T cells. The TCRs are chosen from V beta
CC   6.2/3, V beta 6/5, V beta 6.7, V beta 2, V beta 5/1, V beta 7 or V beta
CC   13. The V beta TCR peptide-based vaccines are useful for prevention or
CC   treatment of multiple sclerosis (MS). The presence of V beta 6.7 appears
CC   to be particularly associated with multiple sclerosis and can be used
CC   to determine an individual's susceptibility to multiple sclerosis.
CC   Vaccinating, rather than passively administering heterologous
CC   antibodies, allows the host's own immune system to mobilize and suppress
CC   auto aggressive T cells.  Therefore, the suppression is persistent and
CC   may involve any and all immunological mechanisms in effecting that
CC   suppression.  Such a multi-faceted response is more effective than
CC   the uni-dimensional suppression achieved by passive administration of
CC   monoclonal antibodies or extant-derived regulatory T cell clones.
CC   AAY23517-34 represent human V beta  proteins that are most frequently
CC   expressed in the cerebrospinal fluid (CFS) of MS patients.
XX
SQ   Sequence   106 AA;


  Query Match             77.1%;  Score 74;  DB 20;  Length 106;
  Best Local Similarity   75.0%;  Pred. No. 0.00014;
  Matches   12;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          | ||| || |:||||
Db     34 cdpisehnrlywyrqt 49


RESULT  13
AAR65450
ID   AAR65450 standard; protein; 113 AA.
XX
AC   AAR65450;
XX
DT   24-MAY-1995  (first entry)
XX
DE   T-cell receptor V-beta HUVB6.1.
XX
KW   T-cell receptor; TCR; T-lymphocyte receptor; variable region;
KW   beta-chain; V-beta; multiple sclerosis; cerebrospinal fluid;
KW   autoimmune disease; lymphoma; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO9425063-A.
XX
PD   10-NOV-1994.
XX
PF   29-APR-1994;   94WO-US04789.
XX
PR   29-APR-1993;   93US-0055006.
XX
PA   (IMMU-) IMMUNE RESPONSE CORP.
PA   (SAND-) SAN DIEGO REGIONAL CANCER CENT.
XX
PI   Brostoff SW,  Carlo DJ,  Gold DP,  Smith LR,  Wilson DB;
XX
DR   WPI; 1994-357913/44.
XX
PT   New vaccine against multiple sclerosis using T-cell receptors -
PT   or fragments of T-cell receptors from the beta chain variable
PT   region; for treating auto:immune disease and lymphoma(s)
XX
PS   Disclosure; Fig. 2A; 43pp; English.
XX
CC   Sequences of the T-cell receptor beta-chain variable region that
CC   were most frequently expressed in cultures from the cerebrospinal
CC   fluid of multiple sclerosis patients are given in AAR65450-67.  A
```

```
CC   peptide based on AAR65450-57 has been used for vaccine development.
XX
SQ   Sequence   113 AA;


  Query Match             77.1%;  Score 74;  DB 15;  Length 113;
  Best Local Similarity   68.8%;  Pred. No. 0.00015;
  Matches   11;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          | ||||| :|:||||:
Db     42 cdpisghtalywyrqs 57


RESULT  14
AAR65455
ID   AAR65455 standard; protein; 113 AA.
XX
AC   AAR65455;
XX
DT   24-MAY-1995  (first entry)
XX
DE   T-cell receptor V-beta HUVB6.7.
XX
KW   T-cell receptor; TCR; T-lymphocyte receptor; variable region;
KW   beta-chain; V-beta; multiple sclerosis; cerebrospinal fluid;
KW   autoimmune disease; lymphoma; vaccine.
XX
OS   Homo sapiens.
XX
PN   WO9425063-A.
XX
PD   10-NOV-1994.
XX
PF   29-APR-1994;   94WO-US04789.
XX
PR   29-APR-1993;   93US-0055006.
XX
PA   (IMMU-) IMMUNE RESPONSE CORP.
PA   (SAND-) SAN DIEGO REGIONAL CANCER CENT.
XX
PI   Brostoff SW,  Carlo DJ,  Gold DP,  Smith LR,  Wilson DB;
XX
DR   WPI; 1994-357913/44.
XX
PT   New vaccine against multiple sclerosis using T-cell receptors
PT   or fragments of T-cell receptors from the beta chain variable
PT   region; for treating auto:immune disease and lymphoma(s)
XX
PS   Disclosure; Fig. 2A; 43pp; English.
XX
CC   Sequences of the T-cell receptor beta-chain variable region that
CC   were most frequently expressed in cultures from the cerebrospinal
CC   fluid of multiple sclerosis patients are given in AAR65450-67.  A
CC   peptide based on AAR65450-57 has been used for vaccine development.
XX
SQ   Sequence   113 AA;


  Query Match             77.1%;  Score 74;  DB 15;  Length 113;
  Best Local Similarity   68.8%;  Pred. No. 0.00015;
  Matches   11;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          | ||||| :|:||||:
Db     42 cdpisghtalywyrqs 57


RESULT  15
AAY23517
ID   AAY23517 standard; Protein; 114 AA.
XX
AC   AAY23517;
XX
DT   02-SEP-1999  (first entry)
XX
DE   Amino acid sequence of human V beta 6.1.
XX
KW   Vaccine; T cell receptor; TCR; T cell; V beta 6.2/3; V beta 6/5;
KW   V beta 6.7; V beta 2; V beta 5/1; V beta 7; V beta 13; V beta 6;
KW   multiple sclerosis.
XX
OS   Homo sapiens.
XX
PN   WO9927957-A1.
XX
PD   10-JUN-1999.
XX
PF   03-DEC-1997;   97WO-US23147.
XX
PR   03-DEC-1997;   97WO-US23147.
XX
PA   (IMMU-) IMMUNE RESPONSE CORP.
PA   (KIMM-) KIMMEL CANCER CENT SIDNEY.
XX
PI   Brostoff SW,  Carlo DJ,  Gold DP,  Smith LR,  Wilson DB;
XX
DR   WPI; 1999-404801/34.
XX
PT   T0 cell receptor peptide-derived vaccines
XX
PS   Example 8; Fig 2A-B; 104pp; English.
XX
CC   The specification describes vaccines which comprise immunologically
CC   effective amounts of T cell receptor (TCR) peptides. The TCRs are
CC   present on the surface of T cells. The TCRs are chosen from V beta
CC   6.2/3, V beta 6/5, V beta 6.7, V beta 2, V beta 5/1, V beta 7 or V beta
CC   13. The V beta TCR peptide-based vaccines are useful for prevention or
CC   treatment of multiple sclerosis (MS). The presence of V beta 6.7 appears
CC   to be particularly associated with multiple sclerosis and can be used
CC   to determine an individual's susceptibility to multiple sclerosis.
CC   Vaccinating, rather than passively administering heterologous
CC   antibodies, allows the host's own immune system to mobilize and suppress
CC   auto aggressive T cells.  Therefore, the suppression is persistent and
CC   may involve any and all immunological mechanisms in effecting that
CC   suppression.  Such a multi-faceted response is more effective than
CC   the uni-dimensional suppression achieved by passive administration of
CC   monoclonal antibodies or extant-derived regulatory T cell clones.
CC   AAY23517-34 represent human V beta  proteins that are most frequently
CC   expressed in the cerebrospinal fluid (CFS) of MS patients.
XX
SQ   Sequence   114 AA;


  Query Match             77.1%;  Score 74;  DB 20;  Length 114;
  Best Local Similarity   68.8%;  Pred. No. 0.00016;
  Matches   11;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          | ||||| :|:||||:
Db     42 cdpisghtalywyrqs 57


Search completed: February  9, 2002, 10:51:05
Job time: 52 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 9, 2002, 10:50:13 ; Search time 12.47 Seconds
(without alignments)
28.874 Million cell updates/sec

Title: US-09-591-789-1
Perfect score: 96
Sequence: 1 CKPISGHNSLFWYRQT 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	96	100.0	16	2	US-08-696-049-1	Sequence 1, Appli
2	96	100.0	102	3	US-08-466-368-9	Sequence 9, Appli
3	74	77.1	310	3	US-08-897-097-4	Sequence 4, Appli
4	74	77.1	311	3	US-08-897-097-3	Sequence 3, Appli
5	74	77.1	314	3	US-08-897-097-1	Sequence 1, Appli
6	65	67.7	92	1	US-08-181-492B-27	Sequence 27, Appl
7	65	67.7	92	5	PCT-US95-00408-27	Sequence 27, Appl
8	56	58.3	82	1	US-08-476-405A-25	Sequence 25, Appl
9	56	58.3	121	4	US-08-341-560B-4	Sequence 4, Appli
10	56	58.3	121	5	PCT-US93-03895-4	Sequence 4, Appli
11	56	58.3	250	4	US-08-341-560B-6	Sequence 6, Appli
12	56	58.3	250	5	PCT-US93-03895-6	Sequence 6, Appli
13	56	58.3	306	4	US-09-082-593-2	Sequence 2, Appli
14	47	49.0	18	1	US-08-476-405A-1	Sequence 1, Appli
15	47	49.0	94	3	US-08-297-395-10	Sequence 10, Appl
16	47	49.0	106	2	US-08-652-558-1	Sequence 1, Appli
17	47	49.0	113	2	US-08-466-860-7	Sequence 7, Appli
18	47	49.0	113	3	US-08-472-040A-7	Sequence 7, Appli
19	47	49.0	113	4	US-08-276-776-7	Sequence 7, Appli
20	47	49.0	113	4	US-08-471-209-7	Sequence 7, Appli
21	47	49.0	154	1	US-08-246-242-7	Sequence 7, Appli
22	47	49.0	391	5	PCT-US95-15696-2	Sequence 2, Appli
23	46	47.9	101	2	US-08-466-860-75	Sequence 75, Appl
24	46	47.9	101	3	US-08-472-040A-75	Sequence 75, Appl
25	46	47.9	101	4	US-08-276-776-75	Sequence 75, Appl
26	46	47.9	101	4	US-08-471-209-75	Sequence 75, Appl
27	46	47.9	113	2	US-08-466-860-9	Sequence 9, Appli
28	46	47.9	113	3	US-08-472-040A-9	Sequence 9, Appli
29	46	47.9	113	4	US-08-276-776-9	Sequence 9, Appli
30	46	47.9	113	4	US-08-471-209-9	Sequence 9, Appli
31	45	46.9	528	3	US-08-904-871-5	Sequence 5, Appli
32	45	46.9	748	3	US-08-904-871-6	Sequence 6, Appli
33	45	46.9	748	3	US-08-904-871-13	Sequence 13, Appl
34	44	45.8	248	4	US-08-341-560B-8	Sequence 8, Appli
35	44	45.8	248	5	PCT-US93-03895-8	Sequence 8, Appli
36	44	45.8	293	6	5189147-3	Patent No. 5189147
37	43	44.8	107	5	PCT-US94-07659-8	Sequence 8, Appli
38	43	44.8	1095	4	US-09-112-096-15	Sequence 15, Appl
39	42	43.8	106	2	US-08-652-558-48	Sequence 48, Appl
40	42	43.8	153	2	US-08-652-558-41	Sequence 41, Appl
41	41	42.7	17	2	US-08-454-236-10	Sequence 10, Appl
42	41	42.7	90	2	US-08-454-236-4	Sequence 4, Appli
43	41	42.7	112	2	US-08-454-236-3	Sequence 3, Appli
44	41	42.7	119	4	US-08-477-347-11	Sequence 11, Appl
45	41	42.7	120	4	US-08-341-560B-2	Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-08-696-049-1
; Sequence 1, Application US/08696049
; Patent No. 5911990
; GENERAL INFORMATION:
;   APPLICANT: Marchalonis, John J.
;   APPLICANT: Watson, Ronald R.
;   APPLICANT: Dehghanpisheh, Keivan
;   APPLICANT: Wang, Yuejian
;   APPLICANT: Huang, Dennis S.
;   TITLE OF INVENTION: T-Cell Receptor Peptides and Methods for
;   TITLE OF INVENTION: Preventing the Progression to AIDS in an Animal Model
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Arnold, White & Durkee
;     STREET: P.O. Box 4433
;     CITY: Houston
;     STATE: Texas
;     COUNTRY: USA
;     ZIP: 77210
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/696,049
;     FILING DATE: Concurrently Herewith
;     CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Kammerer, Patricia A.
;     REGISTRATION NUMBER: 29,775
;     REFERENCE/DOCKET NUMBER: ARIZ:002
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 713/787-1400
;     TELEFAX: 713-789-2679
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 16 amino acids
;     TYPE: amino acid
;     STRANDEDNESS:
;     TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-696-049-1


  Query Match 100.0%; Score 96; DB 2; Length 16;
  Best Local Similarity 100.0%; Pred. No. 6.9e-10;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 CKPISGHNSLFWYRQT 16
          ||||||||||||||||
Db      1 CKPISGHNSLFWYRQT 16


RESULT   2
US-08-466-368-9
; Sequence 9, Application US/08466368
; Patent No. 6093539
;  GENERAL INFORMATION:
;    APPLICANT:  Maddon, Paul J.
;    APPLICANT:  Littman, Dan R.
;    APPLICANT:  Chess, Leonard
;    APPLICANT:  Axel, Richard
;    APPLICANT:  Weiss, Robin
;    APPLICANT:  McDougal, J. S.
;    TITLE OF INVENTION:  DNA ENCODING THE T CELL SURFACE PROTEIN
;    TITLE OF INVENTION:  T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT OF AIDS
;    NUMBER OF SEQUENCES:  21
     CORRESPONDENCE ADDRESS:
       ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/466,368
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  24577-E1-B/JPW/AKC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  212-278-0400
;      TELEFAX:  212-391-0525
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  102 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
       TOPOLOGY:  linear
     MOLECULE TYPE:  protein
     HYPOTHETICAL:  YES
;    ANTI-SENSE:  YES
;    FEATURE:
;      NAME/KEY:  Active-site
;      LOCATION:  1..102
US-08-466-368-9


  Query Match            100.0%;  Score 96;  DB 3;  Length 102;
  Best Local Similarity  100.0%;  Pred. No. 5.2e-09;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
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Db     23 CKPISGHNSLFWYRQT 38


RESULT   3
US-08-897-097-4
; Sequence 4, Application US/08897097
; Patent No. 6054292
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  T-CELL RECEPTOR BETA-LIKE PROTEIN
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/897,097
;      FILING DATE:  Herewith
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0346 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  310 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  339012
US-08-897-097-4


  Query Match            77.1%;  Score 74;  DB 3;  Length 310;
  Best Local Similarity  75.0%;  Pred. No. 8e-05;
  Matches   12;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          | |||.|| |:|||||
Db     42 CDPISEHNRLYWYRQT 57


RESULT   4
US-08-897-097-3
; Sequence 3, Application US/08897097
; Patent No. 6054292
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  T-CELL RECEPTOR BETA-LIKE PROTEIN
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/897,097
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;       FILING DATE:  Herewith
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0346 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  311 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       LIBRARY:  GenBank
;       CLONE:  1100182
US-08-897-097-3


  Query Match             77.1%;  Score 74;  DB 3;  Length 311;
  Best Local Similarity   75.0%;  Pred. No. 8.1e-05;
  Matches   12;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
           | ||| || |:|||||
Db      42 CDPISEHNRLYWYRQT 57


RESULT   5
US-08-897-097-1
; Sequence 1, Application US/08897097
; Patent No. 6054292
;  GENERAL INFORMATION:
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  T-CELL RECEPTOR BETA-LIKE PROTEIN
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
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;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/897,097
;      FILING DATE:  Herewith
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0346 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  314 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  TONGTUT01
;      CLONE:  983910
US-08-897-097-1


  Query Match             77.1%;  Score 74;  DB 3;  Length 314;
  Best Local Similarity   68.8%;  Pred. No. 8.1e-05;
  Matches   11;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
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Db      42 CDPISGHTALYWYRQS 57


RESULT   6
US-08-181-492B-27
; Sequence 27, Application US/08181492B
; Patent No. 5552300
;  GENERAL INFORMATION:
;    APPLICANT:  Makrides, Savvas C
;    APPLICANT:  Kung, Patrick C
;    TITLE OF INVENTION:  T Cell Antigen Receptor V Region     Proteins and Meth
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  T Cell Sciences, Inc.
;      STREET:  115 Fourth Avenue
;      CITY:  Needham
;      STATE:  Massachusetts
;      COUNTRY:  United States of America
;      ZIP:  02194-2725
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44Mb storage
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  MS-DOS 6.2
;      SOFTWARE:  WordPerfect 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/181,492B
;      FILING DATE:  13-January-1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Yankwich, Leon R.
;      REGISTRATION NUMBER:  30,237
;      REFERENCE/DOCKET NUMBER:  TCS-203-P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-345-9100
;      TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  92 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
US-08-181-492B-27


  Query Match             67.7%;  Score 65;  DB 1;  Length 92;
  Best Local Similarity   66.7%;  Pred. No. 0.00067;
  Matches   10;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQ 15
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Db      21 CSPISGHKSVSWYQQ 35


RESULT   7
PCT-US95-00408-27
; Sequence 27, Application PC/TUS9500408
;  GENERAL INFORMATION:
;    APPLICANT:  T.Cell Sciences, Inc
;    TITLE OF INVENTION:  T Cell Antigen Receptor V Region Proteins
;    TITLE OF INVENTION:  and Methods of Preparation Thereof
;    NUMBER OF SEQUENCES:  29
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  T Cell Sciences, Inc.
;      STREET:  1515 Fourth Avenue
;      CITY:  Needham
;      STATE:  Massachusetts
;      COUNTRY:  United States of America
;      ZIP:  02194-2725
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.50 inch, 1.44Mb storage
;      COMPUTER:  IBM PC Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/00408
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/181,492
;      FILING DATE:  13-January-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  YANKWICH, Leon R
;      REGISTRATION NUMBER:  30,237
;      REFERENCE/DOCKET NUMBER:  TCS-203-PCT(94,664-A)
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-345-9100
;      TELEFAX:  617-345-9111
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  92 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:
;    ANTI-SENSE:
;    FEATURE:
;      NAME/KEY:
;      LOCATION:
:T-US95-00408-27


  Query Match             67.7%;  Score 65;  DB 5;  Length 92;
  Best Local Similarity   66.7%;  Pred. No. 0.00067;
  Matches   10;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQ 15
           | ||||| |: ||:|
Db      21 CSPISGHKSVSWYQQ 35


RESULT   8
US-08-476-405A-25
; Sequence 25, Application US/08476405A
; Patent No. 5776459
;  GENERAL INFORMATION:
;    APPLICANT:  Vandenbark, Arthur A.
;    TITLE OF INVENTION:  Method of Treatment Using TCR VBeta5 Peptides
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Connective Therapeutics, Inc.
;      STREET:  3400 West Bayshore Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,405A
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/059,020
;      FILING DATE:  16-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/735,612
;      FILING DATE:  16-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/708,022
;      FILING DATE:  31-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/554,529
;      FILING DATE:  19-JUL-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/467,577
;      FILING DATE:  19-JAN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/382,804
;      FILING DATE:  19-JUL-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lowin, David A.
;      REGISTRATION NUMBER:  29,326
;      REFERENCE/DOCKET NUMBER:  886 P15
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-2800
;      TELEFAX:  415-843-2899
;  INFORMATION FOR SEQ ID NO:  25:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  82 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-476-405A-25


  Query Match             58.3%;  Score 56;  DB 1;  Length 82;
  Best Local Similarity   53.3%;  Pred. No. 0.019;
  Matches    8;  Conservative    4;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQ 15
           | | |||::: ||:|
Db      11 CSPKSGHDTVSWYQQ 25


RESULT   9
US-08-341-560B-4
; Sequence 4, Application US/08341560B
; Patent No. 6165745
;  GENERAL INFORMATION:
;    APPLICANT:  Ward, E. Sally
;    APPLICANT:  Kim, Jin-Kyoo
;    TITLE OF INVENTION:  Recombinant Production of
;    TITLE OF INVENTION:  Immunoglobin-Like Domains in Prokaryotic Cells
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  7721-4433
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/341,560B
;      FILING DATE:  17-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/963,333
;      FILING DATE:  19-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/873,930
;      FILING DATE:  24-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parker, David L.
;      REGISTRATION NUMBER:  32,165
;      REFERENCE/DOCKET NUMBER:  UTSD:353
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (713) 789-2679
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  121 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-341-560B-4


  Query Match             58.3%;  Score 56;  DB 4;  Length 121;
  Best Local Similarity   46.7%;  Pred. No. 0.029;
  Matches    7;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQ 15
           |   : ||:::|||| 
Db      23 CNQTNNHNNMYWYRQ 37


RESULT  10
PCT-US93-03895-4
; Sequence 4, Application PC/TUS9303895
;  GENERAL INFORMATION:
;    APPLICANT:  BOARD OF REGENTS, THE UNIVERSITY
;    APPLICANT:  OF TEXAS SYSTEM
;    APPLICANT:  WARD, Elizabeth Sally and KIM, Jin-Kyoo
;    TITLE OF INVENTION:  RECOMBINANT PRODUCTION OF
;    TITLE OF INVENTION:  IMMUNOGLOBULIN-LIKE DOMAINS IN
;    TITLE OF INVENTION:  PROKARYOTIC CELLS
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
;      STATE:  TEXAS
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/03895
;      FILING DATE:  19930426
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KITCHELL, BARBARA S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  UTFD353PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512-320-7200
;      TELEFAX:  512-474-7577
;      TELEX:  79-0924
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  121 amino acid residues
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US93-03895-4


  Query Match             58.3%;  Score 56;  DB 5;  Length 121;
  Best Local Similarity   46.7%;  Pred. No. 0.029;
  Matches    7;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQ 15
           |   : ||:::|||| 
Db      23 CNQTNNHNNMYWYRQ 37


RESULT  11
US-08-341-560B-6
; Sequence 6, Application US/08341560B
; Patent No. 6165745
;  GENERAL INFORMATION:
;    APPLICANT:  Ward, E. Sally
;    APPLICANT:  Kim, Jin-Kyoo
;    TITLE OF INVENTION:  Recombinant Production of
;    TITLE OF INVENTION:  Immunoglobin-Like Domains in Prokaryotic Cells
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. Box 4433
;      CITY:  Houston
;      STATE:  Texas
;      COUNTRY:  USA
;      ZIP:  7721-4433
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/341,560B
;      FILING DATE:  17-NOV-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/963,333
;      FILING DATE:  19-OCT-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/873,930
;      FILING DATE:  24-APR-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Parker, David L.
;      REGISTRATION NUMBER:  32,165
;      REFERENCE/DOCKET NUMBER:  UTSD:353
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (512) 418-3000
;      TELEFAX:  (713) 789-2679
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-341-560B-6


  Query Match             58.3%;  Score 56;  DB 4;  Length 250;
  Best Local Similarity   46.7%;  Pred. No. 0.063;
  Matches    7;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQ 15
```

```
          |   : ||:::||||
Db    152 CNQTNNHNNMYWYRQ 166


RESULT 12
PCT-US93-03895-6
; Sequence 6, Application PC/TUS9303895
;  GENERAL INFORMATION:
;    APPLICANT:  BOARD OF REGENTS, THE UNIVERSITY
;    APPLICANT:  OF TEXAS SYSTEM
;    APPLICANT:  WARD, Elizabeth Sally and KIM, Jin-Kyoo
;    TITLE OF INVENTION:  RECOMBINANT PRODUCTION OF
;    TITLE OF INVENTION:  IMMUNOGLOBULIN-LIKE DOMAINS IN
;    TITLE OF INVENTION:  PROKARYOTIC CELLS
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ARNOLD, WHITE & DURKEE
;      STREET:  P.O. BOX 4433
;      CITY:  HOUSTON
;      STATE:  TEXAS
;      COUNTRY:  USA
;      ZIP:  77210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/03895
;      FILING DATE:  19930426
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  KITCHELL, BARBARA S.
;      REGISTRATION NUMBER:  33,928
;      REFERENCE/DOCKET NUMBER:  UTFD353PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  512-320-7200
;      TELEFAX:  512-474-7577
;      TELEX:  79-0924
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  250 amino acid residues
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US93-03895-6


  Query Match             58.3%;  Score 56;  DB 5;  Length 250;
  Best Local Similarity   46.7%;  Pred. No. 0.063;
  Matches    7;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQ 15
          |   : ||:::||||
Db    152 CNQTNNHNNMYWYRQ 166


RESULT 13
US-09-082-593-2
; Sequence 2, Application US/09082593
; Patent No. 6180104
; GENERAL INFORMATION:
;  APPLICANT: DAVIS, MARK M.
;  APPLICANT: HEDRICK, STEPHEN M.
;  TITLE OF INVENTION: T CELL RECEPTOR BETA SUBUNIT
;  FILE REFERENCE: JX1193-195DIV2
;  CURRENT APPLICATION NUMBER: US/09/082,593
;  CURRENT FILING DATE: 1998-05-20
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 306
;   TYPE: PRT
;   ORGANISM: Mus musculus
US-09-082-593-2


  Query Match             58.3%;  Score 56;  DB 4;  Length 306;
  Best Local Similarity   43.8%;  Pred. No. 0.078;
  Matches    7;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          |:   |||:::||:|:
Db     41 CEQHLGHNAMYWYKQS 56


RESULT 14
US-08-476-405A-1
; Sequence 1, Application US/08476405A
; Patent No. 5776459
;  GENERAL INFORMATION:
;    APPLICANT:  Vandenbark, Arthur A.
;    TITLE OF INVENTION:  Method of Treatment Using TCR VBeta5 Peptides
;    NUMBER OF SEQUENCES:  27
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Connective Therapeutics, Inc.
;      STREET:  3400 West Bayshore Road
;      CITY:  Palo Alto
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/476,405A
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/059,020
;      FILING DATE:  16-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/735,612
;      FILING DATE:  16-JUL-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/708,022
;      FILING DATE:  31-MAY-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/554,529
;      FILING DATE:  19-JUL-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/467,577
;      FILING DATE:  19-JAN-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/382,804
;      FILING DATE:  19-JUL-1989
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lowin, David A.
;      REGISTRATION NUMBER:  29,326
;      REFERENCE/DOCKET NUMBER:  886 P15
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-843-2800
;      TELEFAX:  415-843-2899
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-476-405A-1


  Query Match             49.0%;  Score 47;  DB 1;  Length 18;
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  Best Local Similarity   53.8%;  Pred. No. 0.11;
  Matches    7;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       3 PISGHNSLFWYRQ 15
           | |||::: ||:|
Db       1 PKSGHDTVSWYQQ 13


RESULT  15
US-08-297-395-10
; Sequence 10, Application US/08297395A
; Patent No. 6039947
; GENERAL INFORMATION:
;  APPLICANT: Howard L. Weiner
;  APPLICANT: David A. Hafler
;  TITLE OF INVENTION: PEPTIDES DERIVED FROM IMMUNODOMINANT
;  TITLE OF INVENTION: EPITOPES OF MYELIN BASIC PROTEIN
;  FILE REFERENCE: 1010/05723US3
;  CURRENT APPLICATION NUMBER: US/08/297,395A
:  CURRENT FILING DATE: 1994-08-11
   EARLIER APPLICATION NUMBER: 08/059,189
;  EARLIER FILING DATE: 1993-05-06
;  EARLIER APPLICATION NUMBER: 07/502,559
;  EARLIER FILING DATE: 1990-03-30
;  EARLIER APPLICATION NUMBER: PCT/US88/02139
;  EARLIER FILING DATE: 1988-06-24
;  EARLIER APPLICATION NUMBER: 07/065,734
;  EARLIER FILING DATE: 1987-06-24
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 10
;   LENGTH: 94
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-297-395-10


  Query Match            49.0%;  Score 47;  DB 3;  Length 94;
  Best Local Similarity  40.0%;  Pred. No. 0.68;
  Matches    6;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQ 15
           |:    |::::|||| 
Db      23 CEQNLNHDAMYWYRQ 37


Search completed: February  9, 2002, 10:51:25
Job time: 72 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 9, 2002, 10:50:13 ; Search time 12.99 Seconds
(without alignments)
93.825 Million cell updates/sec

Title: US-09-591-789-1
Perfect score: 96
Sequence: 1 CKPISGHNSLFWYRQT 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	96	100.0	114	2	I38314	T-cell receptor be
2	96	100.0	115	2	S03510	T-cell receptor be
3	96	100.0	135	1	RWHUVY	T-cell receptor be
4	96	100.0	135	2	S57877	T cell receptor CK
5	87	90.6	134	2	I71938	MHC class II I-A-b
6	85	88.5	93	2	S03488	T-cell receptor be
7	85	88.5	114	2	I38315	T-cell receptor be
8	85	88.5	115	2	S03511	T-cell receptor be
9	85	88.5	133	2	S57870	T cell receptor Ck
10	81	84.4	114	2	A27553	T-cell receptor be
11	81	84.4	134	1	RWMSB3	T-cell receptor be
12	81	84.4	145	2	S21651	T-cell receptor be
13	81	84.4	307	1	RWMSBC	T-cell receptor be
14	80	83.3	114	2	S17379	T-cell receptor be
15	80	83.3	114	2	I38316	T-cell receptor be
16	80	83.3	115	2	S03513	T-cell receptor be
17	77	80.2	115	2	A30995	T-cell receptor be
18	74	77.1	38	2	PL0229	T-cell receptor be
19	74	77.1	61	2	S30440	T-cell receptor be
20	74	77.1	79	2	S17389	T-cell receptor be
21	74	77.1	84	2	I38310	T-cell receptor be
22	74	77.1	91	2	PL0227	T-cell receptor be
23	74	77.1	93	2	A27590	T-cell receptor be
24	74	77.1	101	2	I32537	T-cell receptor be
25	74	77.1	106	2	H32537	T-cell receptor be
26	74	77.1	114	2	PT0733	T-cell receptor be
27	74	77.1	114	2	PT0734	T-cell receptor be
28	74	77.1	114	2	S17387	T-cell receptor be
29	74	77.1	115	2	S22035	T-cell receptor be
30	74	77.1	115	2	S22038	T-cell receptor be
31	74	77.1	129	2	S57884	T cell receptor WI
32	74	77.1	132	2	S30441	T-cell receptor be
33	74	77.1	133	1	RWHU7B	T-cell receptor be
34	74	77.1	135	2	S38386	T-cell receptor be
35	74	77.1	135	2	S57882	T cell receptor PS
36	74	77.1	139	2	S38393	T-cell receptor be
37	74	77.1	141	2	S03495	T-cell receptor be
38	74	77.1	151	2	S24064	T-cell receptor be
39	73	76.0	102	2	S03492	T-cell receptor be
40	73	76.0	106	2	S25416	T-cell receptor be
41	73	76.0	113	2	S22039	T-cell receptor be
42	73	76.0	114	2	S17388	T-cell receptor be
43	73	76.0	114	2	I38313	T-cell receptor be
44	73	76.0	140	2	S36942	T-cell receptor be
45	72	75.0	114	2	G32537	T-cell receptor be

ALIGNMENTS

RESULT 1
I38314
T-cell receptor beta chain V region (V-beta 8.1, germline) precursor - human (fr
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jan-2000
C;Accession: I38314
R;Slightom, J.L.; Siemieniak, D.R.; Sieu, L.C.; Koop, B.F.; Hood, L.
Genomics 20, 149-168, 1994
A;Title: Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell rece
A;Reference number: A54302; MUID:94292194
A;Accession: I38314
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <RES>
A;Cross-references: EMBL:U03115; NID:g467918; PIDN:AAA17713.1; PID:g467923
C;Genetics:
A;Gene: TCRBV8S1
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;35-113/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 96; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy       1 CKPISGHNSLFWYRQT 16
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Db      42 CKPISGHNSLFWYRQT 57
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RESULT 2
S03510
T-cell receptor beta chain precursor V region (8.1) - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C;Accession: S03510; S03512
R;Siu, G.; Strauss, E.C.; Lai, E.; Hood, L.E.
J. Exp. Med. 164, 1600-1614, 1986
A;Title: Analysis of a human V-beta gene subfamily.
A;Reference number: S03510; MUID:87035436
A;Accession: S03510
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-115 <SIU>
A;Cross-references: EMBL:X07192
A;Note: this sequence was determined from the germline gene
R;Smith, W.J.; Tunnacliffe, A.; Rabbitts, T.H.
Nucleic Acids Res. 15, 4991, 1987
A;Title: Germline sequence of two human T-cell receptor V-beta genes: V-beta-8.1
A;Reference number: S00520; MUID:87259979

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A;Accession: S03512
A;Molecule type: DNA
A;Residues: 1-10 <SMI>
A;Note: this sequence was determined from the germline gene
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-115/Product: T-cell receptor beta chain (fragment) #status predicted <MAT>
F;22-115/Domain: V region (V-beta 8.1) #status predicted <VRE>
F;35-113/Domain: immunoglobulin homology <IMM>


  Query Match             100.0%;  Score 96;  DB 2;  Length 115;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
           ||||||||||||||||
Db      42 CKPISGHNSLFWYRQT 57


RESULT   3
RWHUVY
T-cell receptor beta chain precursor V region (YT35) - human
N;Alternate names: T-cell receptor beta-1 chain J-B1.2 segment
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 22-Jun-1999
C;Accession: A02000; E24687
R;Yanagi, Y.; Yoshikai, Y.; Leggett, K.; Clark, S.P.; Aleksander, I.; Mak, T.W.
Nature 308, 145-149, 1984
A;Title: A human T cell-specific cDNA clone encodes a protein having extensive homology
A;Reference number: A93324; MUID:84142269
A;Accession: A02000
A;Molecule type: mRNA
A;Residues: 1-135 <YAN>
A;Cross-references: GB:K01571
A;Experimental source: clone YT35
R;Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A;Title: Organization and sequences of the diversity, joining, and constant region genes
A;Reference number: A94081; MUID:86094276
A;Accession: E24687
A;Molecule type: DNA
A;Residues: 121-135 <TOY>
A;Cross-references: GB:M14158; NID:g338844; PIDN:AAA60669.1; PID:g553682
C;Genetics:
 ;Gene: GDB:TCRB
 ;Cross-references: GDB:120405; OMIM:186930
A;Map position: 7q35-7q35
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; receptor; T-cell
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-135/Product: T-cell receptor beta chain V region YT35 #status predicted <MAT>
F;35-113/Domain: immunoglobulin homology <IMM>
F;42-111/Disulfide bonds: #status predicted
F;90/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             100.0%;  Score 96;  DB 1;  Length 135;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
           ||||||||||||||||
Db      42 CKPISGHNSLFWYRQT 57


RESULT   4
S57877
T cell receptor CK14 beta chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C;Accession: S57877
R;Giegerich, G.; Pette, M.; Meinl, E.; Epplen, J.T.; Wekerle, H.; Hinkkanen, A.
Eur. J. Immunol. 22, 753-758, 1992
A;Title: Diversity of T cell receptor alpha and beta chain genes expressed by hur
A;Reference number: S57869; MUID:92192091
A;Accession: S57877
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-135 <GIE>
A;Cross-references: EMBL:X58324; NID:g643002; PIDN:CAA41236.1; PID:g643003
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;35-113/Domain: immunoglobulin homology <IMM>


  Query Match             100.0%;  Score 96;  DB 2;  Length 135;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-08;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
           ||||||||||||||||
Db      42 CKPISGHNSLFWYRQT 57


RESULT   5
I71938
MHC class II I-A-beta protein precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: I71938
R;Spinella, D.G.; Hansen, T.H.; Walsh, W.D.; Behlke, M.A.; Tillinghast, J.P.; Cho
J. Immunol. 138, 3991-3995, 1987
A;Title: Receptor diversity of insulin-specific T cell lines from C57BL (H-2b) mi
A;Reference number: I55978; MUID:87224052
A;Accession: I71938
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-134 <RES>
A;Cross-references: GB:M16681; NID:g199473; PIDN:AAA39626.1; PID:g199474
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;35-113/Domain: immunoglobulin homology <IMM>


  Query Match             90.6%;  Score 87;  DB 2;  Length 134;
  Best Local Similarity   81.2%;  Pred. No. 5e-07;
  Matches   13;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
           |:|:|||| |||||||
Db      42 CEPVSGHNDLFWYRQT 57


RESULT   6
S03488
T-cell receptor beta chain precursor V region (clone HBP41) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 30-May-1997
C;Accession: S03488
R;Kimura, N.; Toyonaga, B.; Yoshikai, Y.; Triebel, F.; Debre, P.; Minden, M.D.; M
J. Exp. Med. 164, 739-750, 1986
A;Title: Sequences and diversity of human T cell receptor beta chain variable reg
A;Reference number: S03485; MUID:86306525
A;Accession: S03488
A;Molecule type: mRNA
A;Residues: 1-93 <KIM>
A;Cross-references: EMBL:X04925
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor


  Query Match             88.5%;  Score 85;  DB 2;  Length 93;
  Best Local Similarity   87.5%;  Pred. No. 7.4e-07;
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```
  Matches   14;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          |||||||: |||||||
Db     42 CKPISGHDYLFWYRQT 57


RESULT   7
I38315
T-cell receptor beta chain V region (V-beta 8.2, germline) precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jan-2000
C;Accession: I38315
R;Slightom, J.L.; Siemieniak, D.R.; Sieu, L.C.; Koop, B.F.; Hood, L.
Genomics 20, 149-168, 1994
A;Title: Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell receptor ger
A;Reference number: A54302; MUID:94292194
A;Accession: I38315
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <RES>
A;Cross-references: EMBL:U03115; NID:g467918; PIDN:AAA17714.1; PID:g467924
C;Genetics:
A;Gene: TCRBV8S2
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;35-113/Domain: immunoglobulin homology <IMM>


  Query Match             88.5%;  Score 85;  DB 2;  Length 114;
  Best Local Similarity   87.5%;  Pred. No. 9e-07;
  Matches   14;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          |||||||: |||||||
Db     42 CKPISGHDYLFWYRQT 57


RESULT   8
S03511
T-cell receptor beta chain V region 8.2 precursor (clone H7.1 and others) - human
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jan-2000
C;Accession: S03511; S78510; S78511; S26270; S26271
R;Siu, G.; Strauss, E.C.; Lai, E.; Hood, L.E.
J. Exp. Med. 164, 1600-1614, 1986
A;Title: Analysis of a human V-beta gene subfamily.
A;Reference number: S03510; MUID:87035436
A;Accession: S03511
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-115 <SIU>
A;Cross-references: EMBL:X07222
A;Experimental source: clone H7.1
A;Genetics: G1
A;Note: this sequence was determined from the germline gene
R;Plaza, A.
submitted to the EMBL Data Library, February 1991
A;Reference number: S78510
A;Accession: S78510
A;Molecule type: mRNA
A;Residues: 1-114 <PLA>
A;Cross-references: EMBL:X57619; NID:g23934; PIDN:CAA40845.1; PID:g23935
A;Experimental source: clone HT2.12
A;Genetics: G2
A;Accession: S78511
A;Molecule type: mRNA
A;Residues: 1,'D',3-114 <PLZ>
A;Cross-references: EMBL:X57720; NID:g23936; PIDN:CAA40887.1; PID:g23937
A;Experimental source: clone HT242
A;Genetics: G3
R;Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
J. Immunol. 147, 4360-4365, 1991
A;Title: New human V-beta genes and polymorphic variants.
A;Reference number: S26255; MUID:92091749
A;Accession: S26270
A;Molecule type: mRNA
A;Residues: 1-96,'R',98-114 <PLW>
A;Cross-references: EMBL:X57619
A;Experimental source: clone HT2.12
A;Genetics: G2
A;Note: the authors translated the codon GGC for residue 2 as Asp
A;Accession: S26271
A;Molecule type: mRNA
A;Residues: 1,'D',3-96,'R',98-114 <PLF>
A;Cross-references: EMBL:X57720
A;Experimental source: clone HT242
A;Genetics: G3
C;Genetics: <G1>
A;Gene: 8.2
A;Introns: 17/1
C;Genetics: <G2>
A;Gene: 8.2a
C;Genetics: <G3>
A;Gene: 8.2b
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-115/Product: T-cell receptor beta chain (fragment) #status predicted <MAT>
F;22-115/Domain: V region (V-beta 8.2) #status predicted <VRE>
F;35-113/Domain: immunoglobulin homology <IMM>


  Query Match             88.5%;  Score 85;  DB 2;  Length 115;
  Best Local Similarity   87.5%;  Pred. No. 9.1e-07;
  Matches   14;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          |||||||: |||||||
Db     42 CKPISGHDYLFWYRQT 57


RESULT   9
S57870
T cell receptor Ck10 beta chain - human
C;Species: Homo sapiens (man)
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C;Accession: S57870
R;Giegerich, G.; Pette, M.; Meinl, E.; Epplen, J.T.; Wekerle, H.; Hinkkanen, A.
Eur. J. Immunol. 22, 753-758, 1992
A;Title: Diversity of T cell receptor alpha and beta chain genes expressed by hur
A;Reference number: S57869; MUID:92192091
A;Accession: S57870
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-133 <GIE>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;35-113/Domain: immunoglobulin homology <IMM>


  Query Match             88.5%;  Score 85;  DB 2;  Length 133;
  Best Local Similarity   87.5%;  Pred. No. 1e-06;
  Matches   14;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          ||||||||| :|||||
Db     42 CKPISGHNSDYWYRQT 57


RESULT  10
A27553
T-cell receptor beta chain precursor V region (VAK) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
```

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C;Accession: A27553
R;Epplen, J.T.; Bartels, F.; Becker, A.; Nerz, G.; Prester, M.; Rinaldy, A.; Simon, M.M.
Proc. Natl. Acad. Sci. U.S.A. 83, 4441-4445, 1986
A;Title: Change in antigen specificity of cytotoxic T lymphocytes is associated with the
A;Reference number: A27553; MUID:86233442
A;Accession: A27553
A;Molecule type: DNA
A;Residues: 1-114 <EPP>
A;Cross-references: GB:L29434; GB:M12775; GB:N00046; NID:g459887; PIDN:AAA40218.1; PID:g
A;Note: this sequence was determined from the germline gene
C;Comment: See entry PIR:A02002.
C;Genetics:
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-114/Product: T-cell receptor beta chain V region VAK #status predicted <VAR>
F;35-113/Domain: immunoglobulin homology <IMM>


  Query Match             84.4%;  Score 81;  DB 2;  Length 114;
  Best Local Similarity   75.0%;  Pred. No. 4e-06;
  Matches   12;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          |:||||||:::||||||
Db     42 CEPISGHSAVFWYRQT 57


RESULT  11
RWMSB3
T-cell receptor beta chain precursor V region (CTL-F3) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 30-May-1997
C;Accession: A02002
R;Chou, H.S.; Behlke, M.A.; Godambe, S.A.; Russell, J.H.; Brooks, C.G.; Loh, D.Y.
EMBO J. 5, 2149-2155, 1986
A;Title: T cell receptor genes in an alloreactive CTL clone: implications for rearrangem
A;Reference number: A91048; MUID:87053852
A;Accession: A02002
A;Molecule type: mRNA
A;Residues: 1-134 <CHO>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; T-cell receptor
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-134/Product: T-cell receptor beta chain precursor V region (CTL-F3) #status predict
F;20-115/Region: V segment
F;35-113/Domain: immunoglobulin homology <IMM>
F;116-119/Region: D segment
F;120-134/Region: J segment
F;42-111/Disulfide bonds: #status predicted
F;90/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             84.4%;  Score 81;  DB 1;  Length 134;
  Best Local Similarity   75.0%;  Pred. No. 4.7e-06;
  Matches   12;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          |:||||||:::||||||
Db     42 CEPISGHSAVFWYRQT 57


RESULT  12
S21651
T-cell receptor beta chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C;Accession: S21651
R;Yamagishi, H.
submitted to the EMBL Data Library, November 1990
A;Reference number: S21643
A;Accession: S21651
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-145 <YAM>
A;Cross-references: EMBL:X56708; NID:g54647; PIDN:CAA40038.1; PID:g54648
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;35-113/Domain: immunoglobulin homology <IMM>


  Query Match             84.4%;  Score 81;  DB 2;  Length 145;
  Best Local Similarity   75.0%;  Pred. No. 5.1e-06;
  Matches   12;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          |:||||||:::||||||
Db     42 CEPISGHSAVFWYRQT 57


RESULT  13
RWMSBC
T-cell receptor beta chain precursor (F5) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Aug-1984 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C;Accession: S03716; S25118; A02134; A93336; B93333
R;Palmer, M.S.; Bentley, A.; Gould, K.; Townsend, A.R.M.
Nucleic Acids Res. 17, 2353, 1989
A;Title: The T cell receptor from an influenza-A specific murine CTL clone.
A;Reference number: S03715; MUID:89202046
A;Accession: S03716
A;Molecule type: mRNA
A;Residues: 1-307 <PAL>
A;Cross-references: EMBL:X14388; NID:g54668; PIDN:CAA32563.1; PID:g54669
R;Austrup, F.; Kodelja, V.; Kucharzik, T.; Klsch, E.
submitted to the EMBL Data Library, July 1992
A;Description: Characterization of idiotype-specific I-Ed-restricted T suppressor
/c mice.
A;Reference number: S25117
A;Accession: S25118
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1,'GIQT',6,'C',8,'VIFYV',14,'I',16,'NH',19,'D',21-23,'T',25-29,'E',31
'K',86,'E',88,'L',90,'S',92,'F',94-99,'P',101,'E',103,'K',105-114,'LDNSAET','LY',
A;Cross-references: EMBL:X67128; NID:g54678; PIDN:CAA47607.1; PID:g54679
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; receptor; T-cell; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-307/Product: T-cell receptor beta chain #status predicted <MAT>
F;158-228/Domain: immunoglobulin homology <IMM>
F;281-302/Domain: transmembrane #status predicted <TMM>
F;303-307/Domain: intracellular #status predicted <INT>


  Query Match             84.4%;  Score 81;  DB 1;  Length 307;
  Best Local Similarity   75.0%;  Pred. No. 1.1e-05;
  Matches   12;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQT 16
          |:||||||:::||||||
Db     42 CEPISGHSAVFWYRQT 57


RESULT  14
S17379
T-cell receptor beta chain V region (clone IGRb02) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S17379
R;Ferradini, L.; Roman-Roman, S.; Azocar, J.; Michalaki, H.; Triebel, F.; Hercend
Eur. J. Immunol. 21, 935-942, 1991
A;Title: Studies on the human T cell receptor alpha/beta variable region genes. I
A;Reference number: S17378; MUID:91209402
A;Accession: S17379
A;Status: preliminary
```

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A;Molecule type: mRNA
A;Residues: 1-114 <FER>
A;Cross-references: EMBL:X58797; NID:g33527; PIDN:CAA41603.1; PID:g33528
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;36-113/Domain: immunoglobulin homology <IMM>


  Query Match             83.3%;  Score 80;  DB 2;  Length 114;
  Best Local Similarity   80.0%;  Pred. No. 5.8e-06;
  Matches   12;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQ 15
           | |||||:|:||||
Db      42 CNPISGHNTLYWYRQ 56


RESULT  15
I38316
T-cell receptor beta chain V region (V-beta 8.3, germline) precursor - human (fragment)
;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jan-2000
C;Accession: I38316
R;Slightom, J.L.; Siemieniak, D.R.; Sieu, L.C.; Koop, B.F.; Hood, L.
Genomics 20, 149-168, 1994
A;Title: Nucleotide sequence analysis of 77.7 kb of the human V beta T-cell receptor gen
A;Reference number: A54302; MUID:94292194
A;Accession: I38316
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <RES>
A;Cross-references: EMBL:U03115; NID:g467918; PIDN:AAA17715.1; PID:g467925
C;Genetics:
A;Gene: TCRBV8S3
A;Introns: 17/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor
F;35-113/Domain: immunoglobulin homology <IMM>


  Query Match             83.3%;  Score 80;  DB 2;  Length 114;
  Best Local Similarity   75.0%;  Pred. No. 5.8e-06;
  Matches   12;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
           |:|| |||::||||||
Db      42 CQPILGHNTVFWYRQT 57


Search completed: February  9, 2002, 10:50:34
Job time: 21 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 9, 2002, 10:51:07 ; Search time 10.2 Seconds
(without alignments)
57.513 Million cell updates/sec

Title: US-09-591-789-1
Perfect score: 96
Sequence: 1 CKPISGHNSLFWYRQT 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	96	100.0	135	1	TVB1_HUMAN	P01733 homo sapien
2	81	84.4	134	1	TVB7_MOUSE	P06320 mus musculu
3	74	77.1	133	1	TVB2_HUMAN	P04435 homo sapien
4	67	69.8	321	1	TCB_FLV	P11364 feline leuk
5	56	58.3	130	1	TVB8_MOUSE	P06321 mus musculu
6	56	58.3	133	1	TVB2_MOUSE	P01735 mus musculu
7	51	53.1	135	1	TVB1_MOUSE	P01734 mus musculu
8	47	49.0	122	1	TVB5_MOUSE	P04213 mus musculu
9	47	49.0	136	1	TVB4_MOUSE	P04212 mus musculu
10	47	49.0	137	1	Y137_ADE02	P03293 human adeno
11	47	49.0	567	1	NU2M_HANWI	P48906 hansenula w
12	45	46.9	748	1	PHY1_SYNY3	Q55168 synechocyst
13	44	45.8	120	1	TVB3_MOUSE	P01736 mus musculu
14	43	44.8	103	1	RPOM_ARCFU	O29033 archaeoglob
15	42	43.8	194	1	VA43_VACCC	P21065 vaccinia vi
16	42	43.8	194	1	VA43_VACCV	P26671 vaccinia vi
17	42	43.8	195	1	VA43_VARV	P33855 variola vir
18	42	43.8	788	1	TRS1_HCMVA	P09695 human cytom
19	42	43.8	846	1	IRS1_HCMVA	P09715 human cytom
20	42	43.8	1129	1	PHYA_PETCR	P55141 petroselinu
21	41	42.7	108	1	RPOM_METJA	Q58548 methanococc
22	41	42.7	492	1	CAT1_MAIZE	P18122 zea mays (m
23	41	42.7	540	1	YFE0_YEAST	P43562 saccharomyc
24	40.5	42.2	1183	1	YNK6_YEAST	P50942 saccharomyc
25	40	41.7	111	1	LV2I_HUMAN	P01712 homo sapien
26	40	41.7	112	1	LV1B_HUMAN	P01700 homo sapien
27	40	41.7	242	1	GUB_BACSU	P04957 bacillus su
28	40	41.7	337	1	LPPB_HAESO	P36685 haemophilus
29	40	41.7	389	1	CHSB_PEA	P51082 pisum sativ
30	39	40.6	107	1	KV6E_MOUSE	P01679 mus musculu
31	39	40.6	288	1	YDIB_ECOLI	P28244 escherichia
32	39	40.6	323	1	A85B_MYCBO	P12942 mycobacteri
33	39	40.6	389	1	CHS1_PEA	Q01286 pisum sativ
34	39	40.6	389	1	CHS2_PEA	Q01287 pisum sativ
35	39	40.6	492	1	CAT1_HORVU	P55307 hordeum vul
36	39	40.6	492	1	CAT2_WHEAT	P55313 triticum ae
37	39	40.6	501	1	XYLB_LACLA	Q9cfg8 lactococcus
38	38	39.6	108	1	KV1C_HUMAN	P01595 homo sapien
39	38	39.6	111	1	LV2D_HUMAN	P01707 homo sapien
40	38	39.6	111	1	LV2F_HUMAN	P01709 homo sapien
41	38	39.6	115	1	KV5C_MOUSE	P01635 mus musculu
42	38	39.6	142	1	VPR1_MOUSE	P13372 mus musculu
43	38	39.6	142	1	VPR2_MOUSE	P13373 mus musculu
44	38	39.6	265	1	CHS7_MEDSA	P51080 medicago sa
45	38	39.6	285	1	CHS6_MEDSA	P51079 medicago sa

ALIGNMENTS

```
RESULT   1
TVB1_HUMAN
ID   TVB1_HUMAN     STANDARD;      PRT;   135 AA.
AC   P01733;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   T-CELL RECEPTOR BETA CHAIN V REGION YT35 PRECURSOR.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84142269; PubMed=6336315;
RA   Yanagi Y., Yoshikai Y., Leggett K., Clark S.P., Aleksander I.,
RA   Mak T.W.;
RT   "A human T cell-specific cDNA clone encodes a protein having
RT   extensive homology to immunoglobulin chains.";
RL   Nature 308:145-149(1984).
DR   PIR; A02000; RWHUVY.
DR   HSSP; P01789; 2MCP.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   T-cell; Receptor; Signal.
FT   SIGNAL        1      ?       POTENTIAL.
FT   CHAIN         ?    135       T-CELL RECEPTOR BETA CHAIN V REGION YT35.
FT   NON_TER     135    135
SQ   SEQUENCE   135 AA;  15097 MW;  9FBF913D33967CC9 CRC64;


  Query Match             100.0%;  Score 96;  DB 1;  Length 135;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-09;
  Matches   16;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
           ||||||||||||||||
Db      42 CKPISGHNSLFWYRQT 57


RESULT   2
TVB7_MOUSE
ID   TVB7_MOUSE     STANDARD;      PRT;   134 AA.
AC   P06320;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   T-CELL RECEPTOR BETA CHAIN V REGION CTL-F3 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
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```
RX   MEDLINE=87053852; PubMed=3490968;
RA   Chou H.S., Behlke M.A., Godambe S.A., Russell J.H., Brooks C.G.,
RA   Loh D.Y.;
RT   "T cell receptor genes in an alloreactive CTL clone: implications for
RT   rearrangement and germline diversity of variable gene segments.";
RL   EMBO J. 5:2149-2155(1986).
DR   PIR; A02002; RWMSB3.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   T-cell; Receptor; Glycoprotein; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    134       T-CELL RECEPTOR BETA CHAIN V REGION CTL-
FT                               F3.
FT   DOMAIN      20    115       V SEGMENT.
FT   DOMAIN     116    119       D SEGMENT.
FT   DOMAIN     120    134       J SEGMENT.
FT   DISULFID    42    111       BY SIMILARITY.
FT   CARBOHYD    90     90       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER    134    134
SQ   SEQUENCE   134 AA;  14946 MW;  C080FB24C81988F6 CRC64;


  Query Match             84.4%;  Score 81;  DB 1;  Length 134;
  Best Local Similarity   75.0%;  Pred. No. 8.5e-07;
  Matches   12;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
           |:||||:::||||||
Db      42 CEPISGHSAVFWYRQT 57


RESULT   3
TVB2_HUMAN
ID   TVB2_HUMAN     STANDARD;      PRT;   133 AA.
AC   P04435;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   T-CELL RECEPTOR BETA CHAIN V REGION CTL-L17 PRECURSOR.
GN   TCRB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
 X   MEDLINE=86276770; PubMed=2426193;
.A   Leiden J.M., Fraser J.D., Strominger J.L.;
RT   "The complete primary structure of the T-cell receptor genes from an
RT   alloreactive cytotoxic human T-lymphocyte clone.";
RL   Immunogenetics 24:17-23(1986).
CC   -!- MISCELLANEOUS: THIS SEQUENCE WAS DERIVED FROM A HUMAN CYTOTOXIC
CC       T-LYMPHOCYTE THAT IS T3+, T4+, T8-.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M15564; AAA61027.1; -.
DR   PIR; A02001; RWHU7B.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   T-cell; Receptor; Glycoprotein; Signal.
FT   SIGNAL       1     21
FT   CHAIN       22    133       T-CELL RECEPTOR BETA CHAIN V REGION CTL-
FT                               L17.
FT   DOMAIN      22    114       V SEGMENT.
FT   DOMAIN     115    118       D SEGMENT.
FT   DOMAIN     119    133       J SEGMENT.
FT   CARBOHYD    30     30       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    37     37       N-LINKED (GLCNAC. . .).
FT   DISULFID    42    111
FT   NON_TER    133    133
SQ   SEQUENCE   133 AA;  14999 MW;  21030818D18D341F CRC64;


  Query Match             77.1%;  Score 74;  DB 1;  Length 133;
  Best Local Similarity   75.0%;  Pred. No. 1.3e-05;
  Matches   12;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
           | ||| || |:|||||
Db      42 CDPISEHNRLYWYRQT 57


RESULT   4
TCB_FLV
ID   TCB_FLV        STANDARD;      PRT;   321 AA.
AC   P11364;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   T-CELL RECEPTOR BETA CHAIN T17T-22 PRECURSOR.
GN   V-TCR.
OS   Feline leukemia virus.
OC   Viruses; Retroid viruses; Retroviridae; Gammaretrovirus.
OX   NCBI_TaxID=11768;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87144638; PubMed=3029597;
RA   Fulton R., Forrest D., McFarlane R., Onions D., Neil J.C.;
RT   "Retroviral transduction of T-cell antigen receptor beta-chain and
RT   myc genes.";
RL   Nature 326:190-194(1987).
RN   [2]
RP   REVISION TO 158-159.
RA   Fulton R.;
RL   Submitted (DEC-1987) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X05155; CAA28801.1; -.
DR   PIR; C26600; RWMVTC.
DR   PIR; B26600; RWMVTV.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003597; Ig_c1.
DR   InterPro; IPR003600; Ig_like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00407; IGc1; 1.
DR   SMART; SM00410; IG_like; 1.
KW   T-cell; Receptor; Transmembrane; Glycoprotein; Signal.
FT   SIGNAL       1     28
FT   CHAIN       29    321       T-CELL RECEPTOR BETA CHAIN T17T-22.
FT   DOMAIN      29    122       V SEGMENT.
FT   DOMAIN     123    128       D SEGMENT.
FT   DOMAIN     129    144       J SEGMENT.
FT   DOMAIN     145    321       C REGION.
SQ   SEQUENCE   321 AA;  35581 MW;  11D2C3BF56811129 CRC64;


  Query Match             69.8%;  Score 67;  DB 1;  Length 321;
  Best Local Similarity   73.3%;  Pred. No. 0.00048;
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  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQ 15
           | ||||| ||:||:|
Db      51 CFPISGHLSLYWYQQ 65


RESULT   5
TVB8_MOUSE
ID   TVB8_MOUSE     STANDARD;      PRT;   130 AA.
AC   P06321;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   T-CELL RECEPTOR BETA CHAIN V REGION A20.2.25 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86068062; PubMed=3906657;
RA   Morinaga T., Fotedar A., Singh B., Wegmann T.G., Tamaoki T.;
RT   "Isolation of cDNA clones encoding a T-cell receptor beta-chain from
RT   a beef insulin-specific hybridoma.";
RL   Proc. Natl. Acad. Sci. U.S.A. 82:8163-8167(1985).
DR   PIR; A02005; RWMS20.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   T-cell; Receptor; Glycoprotein; Signal.
FT   SIGNAL        1     21       BY SIMILARITY.
FT   CHAIN        22   >130       T-CELL RECEPTOR BETA CHAIN V REGION
FT                                A20.2.25.
FT   DOMAIN       22    112       V SEGMENT.
FT   DOMAIN      113    115       D SEGMENT.
FT   DOMAIN      116    130       J SEGMENT.
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     75     75       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   NON_TER     130    130
SQ   SEQUENCE   130 AA;  14732 MW;  6721EC70DC64BEDB CRC64;


  Query Match             58.3%;  Score 56;  DB 1;  Length 130;
  Best Local Similarity   43.8%;  Pred. No. 0.013;
  Matches    7;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
           |:   |||:::||:|:
Db      41 CEQHLGHNAMYWYKQS 56


RESULT   6
TVB2_MOUSE
ID   TVB2_MOUSE     STANDARD;      PRT;   133 AA.
AC   P01735;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   T-CELL RECEPTOR BETA CHAIN V REGION 86T1 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C;
RX   MEDLINE=84142271; PubMed=6546606;
RA   Hedrick S.M., Nielsen E.A., Kavaler J., Cohen D.I., Davis M.M.;
RT   "Sequence relationships between putative T-cell receptor polypeptides
RT   and immunoglobulins.";
RL   Nature 308:153-158(1984).
DR   PIR; A02004; RWMSV8.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   T-cell; Receptor; Glycoprotein; Signal.
FT   SIGNAL        1     21
FT   CHAIN        22    133       T-CELL RECEPTOR BETA CHAIN V REGION 86T1.
FT   DOMAIN       22    113       V SEGMENT.
FT   DOMAIN      114    133       J SEGMENT.
FT   CARBOHYD     36     36       N-LINKED (GLCNAC. . .).
FT   CARBOHYD     75     75       N-LINKED (GLCNAC. . .).
FT   DISULFID     41    109       BY SIMILARITY.
FT   NON_TER     133    133
SQ   SEQUENCE   133 AA;  14986 MW;  73E8E9EBF6F85290 CRC64;


  Query Match             58.3%;  Score 56;  DB 1;  Length 133;
  Best Local Similarity   43.8%;  Pred. No. 0.014;
  Matches    7;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
           |:   |||:::||:|:
Db      41 CEQHLGHNAMYWYKQS 56


RESULT   7
TVB1_MOUSE
ID   TVB1_MOUSE     STANDARD;      PRT;   135 AA.
AC   P01734;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   T-CELL RECEPTOR BETA CHAIN V REGION 3H.25 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85176939; PubMed=2580639;
RA   Goverman J., Minard K., Shastri N., Hunkapiller T., Hansburg D.,
RA   Sercarz E., Hood L.;
RT   "Rearranged beta T cell receptor genes in a helper T cell clone
RT   specific for lysozyme: no correlation between V beta and MHC
RT   restriction.";
RL   Cell 40:859-867(1985).
CC   -!- MISCELLANEOUS: THIS T-CELL CLONE EXPRESSES ONLY A SINGLE V-BETA
CC       CHAIN SEGMENT ALTHOUGH IT HAS THREE REARRANGEMENTS IN THE BETA
CC       CHAIN FAMILY.
CC   -!- MISCELLANEOUS: THIS REARRANGED V-BETA CHAIN SEGMENT, SPECIFIC FOR
CC       CHICKEN EGG-WHITE LYSOZYME AND I-A(B), IS THE SAME AS THAT
CC       EXPRESSED IN A T HELPER CELL SPECIFIC FOR CYTOCHROME C AND AN
CC       I-E(K) MHC MOLECULE.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; M12415; AAA40249.1; -.
DR   PIR; A02003; RWMSBV.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   T-cell; Receptor; Signal.
FT   SIGNAL        1     20
FT   CHAIN        21    135       T-CELL RECEPTOR BETA CHAIN V REGION
FT                                3H.25.
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FT   DOMAIN       21    115       V SEGMENT.
FT   DOMAIN      116    118       D SEGMENT.
FT   DOMAIN      119    135       J SEGMENT.
FT   DISULFID     42    111       BY SIMILARITY.
FT   NON_TER     135    135
SQ   SEQUENCE   135 AA;  15123 MW;  C0FF1DDACF37E76D CRC64;


  Query Match           53.1%;  Score 51;  DB 1;  Length 135;
  Best Local Similarity   53.3%;  Pred. No. 0.098;
  Matches    8;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQ 15
          | |  ||  :|||:|
Db     42 CIPEKGHPVVFWYQQ 56


RESULT   8
TVB5_MOUSE
ID   TVB5_MOUSE     STANDARD;      PRT;   122 AA.
AC   P04213;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   T-CELL RECEPTOR BETA CHAIN V REGION C5 PRECURSOR (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85036636; PubMed=6092964;
RA   Patten P., Yokota T., Rothbard J., Chien Y., Arai K., Davis M.M.;
RT   "Structure, expression and divergence of T-cell receptor beta-chain
RT   variable regions.";
RL   Nature 312:40-46(1984).
CC   -!- MISCELLANEOUS: THIS SEQUENCE WAS DERIVED FROM A T-HELPER CLONE.
DR   PIR; A02008; RWMSC5.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00406; IGv; 1.
KW   T-cell; Receptor; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1      7
FT   CHAIN         8    122       T-CELL RECEPTOR BETA CHAIN V REGION C5.
FT   DOMAIN        8    103       V SEGMENT.
FT   DOMAIN      104    108       D SEGMENT.
FT   DOMAIN      109    122       J SEGMENT.
FT   DISULFID     31     99       BY SIMILARITY.
FT   NON_TER     122    122
SQ   SEQUENCE   122 AA;  13349 MW;  D657DCC9B261C64C CRC64;


  Query Match           49.0%;  Score 47;  DB 1;  Length 122;
  Best Local Similarity   40.0%;  Pred. No. 0.42;
  Matches    6;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQ 15
          |   : |: ::||||
Db     31 CHQTNNHDYMYWYRQ 45


RESULT   9
TVB4_MOUSE
ID   TVB4_MOUSE     STANDARD;      PRT;   136 AA.
AC   P04212;
DT   20-MAR-1987 (Rel. 04, Created)
DT   20-MAR-1987 (Rel. 04, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   T-CELL RECEPTOR BETA CHAIN V REGION LB2 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85036636; PubMed=6092964;
RA   Patten P., Yokota T., Rothbard J., Chien Y., Arai K., Davis M.M.;
RT   "Structure, expression and divergence of T-cell receptor beta-chain
RT   variable regions.";
RL   Nature 312:40-46(1984).
CC   -!- MISCELLANEOUS: THIS SEQUENCE WAS DERIVED FROM A T-HELPER CLONE.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X01643; CAA25800.1; -.
DR   PIR; A02007; RWMSLB.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   T-cell; Receptor; Signal.
FT   SIGNAL        1     21
FT   CHAIN        22    136       T-CELL RECEPTOR BETA CHAIN V REGION LB2.
FT   DOMAIN       22    116       V SEGMENT.
FT   DOMAIN      117    120       D SEGMENT.
FT   DOMAIN      121    136       J SEGMENT.
FT   DISULFID     45    113       BY SIMILARITY.
FT   NON_TER     136    136
SQ   SEQUENCE   136 AA;  15369 MW;  F74D0C0414088D02 CRC64;


  Query Match           49.0%;  Score 47;  DB 1;  Length 136;
  Best Local Similarity   40.0%;  Pred. No. 0.47;
  Matches    6;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQ 15
          |:    |::::||||
Db     45 CQQNFNHDTMYWYRQ 59


RESULT  10
Y137_ADE02
ID   Y137_ADE02     STANDARD;      PRT;   137 AA.
AC   P03293;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   01-APR-1990 (Rel. 14, Last annotation update)
DE   HYPOTHETICAL PROTEIN B-137.
OS   Human adenovirus type 2.
OC   Viruses; dsDNA viruses; no RNA stage; Adenoviridae; Mastadenovirus.
OX   NCBI_TaxID=10515;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83056843; PubMed=7142161;
RA   Gingeras T.R., Sciaky D., Gelinas R.E., Bing-Dong J., Yen C.E.,
RA   Kelly M.M., Bullock P.A., Parsons B.L., O'Neill K.E., Roberts R.J.;
RT   "Nucleotide sequences from the adenovirus-2 genome.";
RL   J. Biol. Chem. 257:13475-13491(1982).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=83056844; PubMed=7142162;
RA   Alestroem P., Akusjaervi G., Pettersson M., Pettersson U.;
RT   "DNA sequence analysis of the region encoding the terminal protein
RT   and the hypothetical N-gene product of adenovirus type 2.";
RL   J. Biol. Chem. 257:13492-13498(1982).
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; J01917; -; NOT_ANNOTATED_CDS.
DR   PIR; A03865; A03865.
KW   Hypothetical protein.
SQ   SEQUENCE   137 AA;  14356 MW;  B7ACA61A63116856 CRC64;


  Query Match             49.0%;  Score 47;  DB 1;  Length 137;
  Best Local Similarity   50.0%;  Pred. No. 0.47;
  Matches    6;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       2 KPISGHNSLFWY 13
           :|:|||:|: |:
Db      60 EPVSGHSSVVWW 71


RESULT  11
NU2M_HANWI
ID   NU2M_HANWI     STANDARD;      PRT;   567 AA.
AC   P48906;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).
GN   ND2.
OS   Hansenula wingei (Yeast).
OG   Mitochondrion.
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Pichia.
OX   NCBI_TaxID=4907;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=21;
RA   Sekito T., Okamoto K., Kitano H., Yoshida K.;
RT   "Yeast Hansenula wingei mitochondria genome's complete DNA sequence
RT   demonstrated unique characteristics.";
RL   Nucleic Acids Symp. Ser. 31:233-234(1994).
CC   -!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC       INNER MEMBRANE.
CC   -!- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 2 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; D31785; BAA06573.1; -.
DR   InterPro; IPR001750; Oxidored_q1.
DR   Pfam; PF00361; oxidored_q1; 1.
KW   Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transmembrane.
SQ   SEQUENCE   567 AA;  66958 MW;  68C0F09B8F8D12BE CRC64;


  Query Match             49.0%;  Score 47;  DB 1;  Length 567;
  Best Local Similarity   88.9%;  Pred. No. 2.1;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       5 SGHNSLFWY 13
           |||||||:|
Db     184 SGHNSLFYY 192


RESULT  12
PHY1_SYNY3
ID   PHY1_SYNY3     STANDARD;      PRT;   748 AA.
AC   Q55168;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   PHYTOCHROME-LIKE PROTEIN CPH1 (EC 2.7.3.-) (LIGHT-REGULATED HISTIDINE
DE   KINASE 1) (BACTERIOPHYTOCHROME CPH1).
GN   CPH1 OR SLR0473.
OS   Synechocystis sp. (strain PCC 6803).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX   NCBI_TaxID=1148;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96127529; PubMed=8590279;
RA   Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA   Sugiura M., Tabata S.;
RT   "Sequence analysis of the genome of the unicellular cyanobacterium
RT   Synechocystis sp. strain PCC6803. 1. Sequence features in the 1 Mb
RT   region from map positions 64% to 92% of the genome.";
RL   DNA Res. 2:153-166(1995).
RN   [2]
RP   CHARACTERIZATION, AND MUTAGENESIS OF HIS-260.
RX   MEDLINE=97426627; PubMed=9278513;
RA   Yeh K.-C., Wu S.-H., Murphy J.T., Lagarias J.C.;
RT   "A cyanobacterial phytochrome two-component light sensory system.";
RL   Science 277:1505-1508(1997).
RN   [3]
RP   CHARACTERIZATION.
RX   MEDLINE=20290819; PubMed=10828948;
RA   Park C.-M., Shim J.-Y., Yang S.-S., Kang J.-G., Kim J.-I., Luka Z.,
RA   Song P.-S.;
RT   "Chromophore-apoprotein interactions in Synechocystis sp. PCC6803
RT   phytochrome Cph1.";
RL   Biochemistry 39:6349-6356(2000).
CC   -!- FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT
CC       ARE REVERSIBLY INTERCONVERTIBLE BY LIGHT: THE R FORM THAT ABSORBS
CC       MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE FR FORM THAT
CC       ABSORBS MAXIMALLY IN THE FAR-RED REGION. HAS ALSO A SLIGHT BLUE
CC       SHIFT FOR THE FAR-RED MAXIMUM. FORMS A TWO-COMPONENT SYSTEM WITH
CC       THE RCP1 RESPONSE REGULATOR.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE (BY
CC       SIMILARITY).
CC   -!- MISCELLANEOUS: THE R FORM EXHIBITS BOTH ATP-DEPENDENT
CC       AUTOPHOSPHORYLATION AND PHOSPHOTRANSFER TO RCP1 ACTIVITIES. UNLIKE
CC       THE HIGHER PLANTS WHERE PFR IS THOUGHT TO BE THE ACTIVE FORM.
CC   -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE PHYTOCHROME
CC       FAMILY.
CC   -!- SIMILARITY: IN THE C-TERMINAL SECTION; TO OTHER PROKARYOTIC
CC       SENSORY TRANSDUCTION HISTIDINE KINASES.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D64001; BAA10307.1; -.
DR   InterPro; IPR000410; Bctrl_sensor.
DR   InterPro; IPR003018; GAF.
DR   InterPro; IPR003594; HATPase_c.
DR   InterPro; IPR003661; His_kinA.
DR   InterPro; IPR000014; PAS.
DR   InterPro; IPR001294; Phytochrome.
DR   Pfam; PF01590; GAF; 1.
DR   Pfam; PF02518; HATPase_c; 1.
DR   Pfam; PF00360; phytochrome; 1.
DR   Pfam; PF00512; signal; 1.
DR   SMART; SM00065; GAF; 1.
DR   SMART; SM00387; HATPase_c; 1.
DR   SMART; SM00388; HisKA; 1.
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DR   SMART; SM00091; PAS; 1.
DR   PROSITE; PS00245; PHYTOCHROME_1; FALSE_NEG.
DR   PROSITE; PS50046; PHYTOCHROME_2; 1.
KW   Sensory transduction; Transferase; Kinase; Phosphorylation;
KW   Photoreceptor; Phytochrome; Chromophore; Complete proteome.
FT   DOMAIN       20     510       CHROMOPHORE BINDING DOMAIN.
FT   DOMAIN      511     748       SENSORY KINASE TRANSMITTER DOMAIN.
FT   BINDING     260     260       CHROMOPHORE (BY SIMILARITY).
FT   MOD_RES     538     538       PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT   MUTAGEN     538     538       H->K: NO AUTOPHOSPHORYLATION; NO
FT                                 PHOSPHOTRANSFER TO RCP1.
SQ   SEQUENCE   748 AA;  84232 MW;  A9ECA6D8D5B3C88A CRC64;


  Query Match             46.9%;  Score 45;  DB 1;  Length 748;
  Best Local Similarity   58.3%;  Pred. No. 6;
  Matches    7;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 PISGHNSLFWYR 14
           ||: || | |:|
Db     430 PIARHNFLLWFR 441


RESULT  13
TVB3_MOUSE
ID   TVB3_MOUSE     STANDARD;      PRT;   120 AA.
AC   P01736;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   T-CELL RECEPTOR BETA CHAIN V REGION PHDS203 PRECURSOR (FRAGMENT).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB.B;
RX   MEDLINE=84245824; PubMed=6330561;
RA   Saito H., Kranz D.M., Takagaki Y., Hayday A.C., Eisen H.N.,
RA   Tonegawa S.;
RT   "Complete primary structure of a heterodimeric T-cell receptor
RT   deduced from cDNA sequences.";
RL   Nature 309:757-762(1984).
CC   -!- MISCELLANEOUS: THIS CLONE WAS ISOLATED FROM A CYTOTOXIC T
CC       LYMPHOCYTE.
DR   PIR; A02006; RWMSV2.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   T-cell; Receptor; Signal.
FT   NON_TER       1      1
FT   SIGNAL       <1     11
FT   CHAIN         12    120       T-CELL RECEPTOR BETA CHAIN V REGION
FT                                 PHDS203.
FT   DOMAIN        12    106       V SEGMENT.
FT   DOMAIN       107    120       J SEGMENT.
FT   DISULFID      34    102       BY SIMILARITY.
FT   NON_TER      120    120
SQ   SEQUENCE   120 AA;  13670 MW;  D6B1011504969DCE CRC64;


  Query Match             45.8%;  Score 44;  DB 1;  Length 120;
  Best Local Similarity   40.0%;  Pred. No. 1.3;
  Matches    6;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQ 15
           |     | :::||||
Db      34 CGQDMSHETMYWYRQ 48


RESULT  14
RPOM_ARCFU
ID   RPOM_ARCFU     STANDARD;      PRT;   103 AA.
AC   O29033;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   DNA-DIRECTED RNA POLYMERASE SUBUNIT M (EC 2.7.7.6).
GN   RPOM OR AF1235.
OS   Archaeoglobus fulgidus.
OC   Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC   Archaeoglobus.
OX   NCBI_TaxID=2234;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX   MEDLINE=98049343; PubMed=9389475;
RA   Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA   Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA   Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA   Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA   Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA   Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA   Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA   Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
RA   Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA   Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA   Venter J.C.;
RT   "The complete genome sequence of the hyperthermophilic, sulphate-
RT   reducing archaeon Archaeoglobus fulgidus.";
RL   Nature 390:364-370(1997).
CC   -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC       OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC       SUBSTRATES.
CC   -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
CC       RNA(N).
CC   -!- SIMILARITY: BELONGS TO THE ARCHAEBACTERIA RPOM / EUKARYOTIC RPA12/
CC       RPB9 / RPC11 RNA POLYMERASE FAMILY.
CC   -!- SIMILARITY: BELONGS TO THE TRANSCRIPTION FACTOR S-II FAMILY.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; AE001019; AAB90009.1; -.
DR   HSSP; Q56254; 1QYP.
DR   TIGR; AF1235; -.
DR   InterPro; IPR001529; RNA_POL_M_15KD.
DR   InterPro; IPR001222; Znf_TFIIS.
DR   Pfam; PF02150; RNA_POL_M_15KD; 1.
DR   Pfam; PF01096; TFIIS; 1.
DR   SMART; SM00440; ZnF_C2C2; 1.
DR   PROSITE; PS00466; TFIIS; 1.
DR   PROSITE; PS01030; RNA_POL_M_15KD; 1.
KW   Transferase; DNA-directed RNA polymerase; Transcription; Zinc-finger;
KW   Complete proteome.
FT   ZN_FING       4     23       C4-TYPE.
FT   ZN_FING      64     95       ZN-RIBBON.
SQ   SEQUENCE   103 AA;  12057 MW;  4C189F2AC1C1B62B CRC64;


  Query Match             44.8%;  Score 43;  DB 1;  Length 103;
  Best Local Similarity   54.5%;  Pred. No. 1.6;
  Matches    6;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 PISGHNSLFWY 13
           |  |||  ||:
Db      65 PACGHNEAFWW 75
```

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RESULT 15
VA43_VACCC
ID   VA43_VACCC     STANDARD;      PRT;   194 AA.
AC   P21065;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   20-AUG-2001 (Rel. 40, Last annotation update)
DE   PROTEIN A43.
GN   A43R.
OS   Vaccinia virus (strain Copenhagen).
OC   Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC   Orthopoxvirus.
OX   NCBI_TaxID=10249;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91021027; PubMed=2219722;
RA   Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA   Paoletti E.;
RT   "The complete DNA sequence of vaccinia virus.";
RL   Virology 179:247-266(1990).
RN   [2]
RP   COMPLETE GENOME.
RA   Goebel S.J., Johnson G.P., Perkus M.E., Davis S.W., Winslow J.P.,
RA   Paoletti E.;
RT   "Appendix to 'The complete DNA sequence of vaccinia virus'.";
RL   Virology 179:517-563(1990).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; M35027; AAA48174.1; -.
DR   PIR; I42521; I42521.
SQ   SEQUENCE   194 AA;  22635 MW;  639990229C05591F CRC64;


  Query Match             43.8%;  Score 42;  DB 1;  Length 194;
  Best Local Similarity   42.9%;  Pred. No. 4.7;
  Matches    6;  Conservative    4;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYR 14
           |  | |::|: ||:
Db     144 CITIIGYDSIIWYK 157



Search completed: February  9, 2002, 10:54:12
Job time: 185 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: February 9, 2002, 10:50:37 ; Search time 23 Seconds
(without alignments)
101.755 Million cell updates/sec

Title: US-09-591-789-1
Perfect score: 96
Sequence: 1 CKPISGHNSLFWYRQT 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	56	58.3	127	11	Q9D3G4	Q9d3g4 mus musculu
2	47	49.0	615	11	O88576	O88576 mus musculu
3	47	49.0	615	11	Q62687	Q62687 rattus norv
4	47	49.0	621	10	Q9FTF3	Q9ftf3 oryza sativ
5	45	46.9	421	10	Q9SY90	Q9sy90 arabidopsis
6	44.5	46.4	981	5	Q9NN63	Q9nn63 leishmania
7	44	45.8	215	11	Q9D2W6	Q9d2w6 mus musculu
8	44	45.8	234	11	Q99N04	Q99n04 mus musculu
9	44	45.8	428	2	Q9L2D5	Q9l2d5 streptomyce
10	44	45.8	556	10	Q9LPW2	Q9lpw2 arabidopsis
11	43	44.8	235	13	Q90770	Q90770 gallus gall
12	43	44.8	331	12	Q98337	Q98337 murine hepa
13	43	44.8	381	10	P94013	P94013 oryza sativ
14	43	44.8	504	8	Q9GF60	Q9gf60 arabis lyal
15	43	44.8	504	8	Q9GF49	Q9gf49 arabis drum
16	43	44.8	504	8	Q9GF48	Q9gf48 arabis lign
17	43	44.8	504	8	Q9GF46	Q9gf46 halimolobos
18	43	44.8	504	8	Q9GF44	Q9gf44 arabis pari
19	43	44.8	504	8	Q9GF43	Q9gf43 arabis drum
20	43	44.8	504	8	Q9GF42	Q9gf42 arabis fend
21	43	44.8	504	8	Q9GF38	Q9gf38 arabidopsis
22	43	44.8	504	8	Q9GF28	Q9gf28 arabidopsis
23	43	44.8	741	10	Q9FJD2	Q9fjd2 arabidopsis
24	42.5	44.3	578	12	Q85314	Q85314 rabbit fibr
25	42.5	44.3	1286	12	Q9Q903	Q9q903 shope fibro
26	42.5	44.3	1286	12	Q9Q8N2	Q9q8n2 myxoma viru
27	42	43.8	190	12	O57244	O57244 vaccinia vi
28	42	43.8	330	12	Q98338	Q98338 murine hepa
29	42	43.8	335	10	Q9M7U6	Q9m7u6 oryza sativ
30	42	43.8	342	2	O84779	O84779 chlamydia t
31	42	43.8	397	4	Q9BYZ7	Q9byz7 homo sapien
32	42	43.8	492	10	Q9SB22	Q9sb22 oryza sativ
33	42	43.8	766	10	Q9LWW1	Q9lww1 oryza sativ
34	42	43.8	769	10	Q9LWV0	Q9lwv0 oryza sativ
35	42	43.8	786	10	Q9LWW2	Q9lww2 oryza sativ
36	42	43.8	1360	12	Q9IKD1	Q9ikd1 rat sialoda
37	42	43.8	1361	12	P90210	P90210 murine hepa
38	41.5	43.2	133	11	Q64094	Q64094 mus musculu
39	41.5	43.2	279	4	Q9HAC3	Q9hac3 homo sapien
40	41.5	43.2	713	4	O95381	O95381 homo sapien
41	41.5	43.2	947	4	Q9HCD6	Q9hcd6 homo sapien
42	41	42.7	279	2	Q9PPH7	Q9pph7 campylobact
43	41	42.7	330	12	Q98340	Q98340 murine hepa
44	41	42.7	330	12	Q98341	Q98341 murine coro
45	41	42.7	407	5	Q9N5S9	Q9n5s9 caenorhabdi

ALIGNMENTS

RESULT 1
Q9D3G4
ID Q9D3G4 PRELIMINARY; PRT; 127 AA.
AC Q9D3G4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE 5830405F06RIK PROTEIN.
GN 5830405F06RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=THYMUS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AK017898; BAB30995.1; -.
DR MGD; MGI:1923265; 5830405F06Rik.
DR InterPro; IPR003599; Ig.

```
DR   InterPro; IPR003600; Ig_like.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00410; IG_like; 1.
SQ   SEQUENCE   127 AA;  14449 MW;  BBEE374302FBDB81 CRC64;


  Query Match           58.3%;  Score 56;  DB 11;  Length 127;
  Best Local Similarity  43.8%;  Pred. No. 0.054;
  Matches    7;  Conservative    6;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       1 CKPISGHNSLFWYRQT 16
           |:   |||:::||:|:
Db      48 CEQHLGHNAMYWYKQS 63


RESULT   2
O88576
ID   O88576      PRELIMINARY;      PRT;   615 AA.
AC   O88576; O88577; O88578; O88579; O88580; O88581;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER XTRP2.
GN   XTRP2 OR XT2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.
RC   TISSUE=KIDNEY;
RX   MEDLINE=99131080; PubMed=9932288;
RA   Nash S.R., Giros B., Kingsmore S.F., Kim K.M., El-Mestikawy S.,
RA   Dong Q., Fumagalli F., Seldin M.F., Caron M.G.;
RT   "Cloning, gene structure, and genomic localization of an orphan
RT   transporter from mouse kidney with six alternatively-spliced
RT   isoforms.";
RL   Recept. Channels 6:113-128(1998).
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC   -!- ALTERNATIVE PRODUCTS: 6 ISOFORMS; A12 (SHOWN HERE), A11, B11, A10,
CC       B9 AND A8; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN KIDNEY.
CC   -!- SIMILARITY: BELONGS TO THE SODIUM:NEUROTRANSMITTER SYMPORTER
CC       FAMILY (SNF).
DR   EMBL; AF075262; AAC27757.1; -.
DR   EMBL; AF075263; AAC27758.1; -.
DR   EMBL; AF075264; AAC27759.1; -.
DR   EMBL; AF075265; AAC27760.1; -.
DR   EMBL; AF075266; AAC27761.1; -.
DR   EMBL; AF075267; AAC27762.1; -.
DR   MGD; MGI:1336892; Xtrp2.
DR   InterPro; IPR000175; Na_neurotran_symport.
DR   Pfam; PF00209; SNF; 1.
DR   PRINTS; PR00176; NANEUSMPORT.
DR   PROSITE; PS00610; NA_NEUROTRAN_SYMP_1; FALSE_NEG.
DR   PROSITE; PS00754; NA_NEUROTRAN_SYMP_2; FALSE_NEG.
DR   PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
KW   Neurotransmitter transport; Transport; Transmembrane; Glycoprotein;
KW   Symport; Alternative splicing.
FT   DOMAIN       1     26       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    27     47       1 (POTENTIAL).
FT   DOMAIN      48     52       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    53     73       2 (POTENTIAL).
FT   DOMAIN      74     83       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    84    104       3 (POTENTIAL).
FT   DOMAIN     105    105       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   106    126       4 (POTENTIAL).
FT   DOMAIN     127    177       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   178    198       5 (POTENTIAL).
FT   DOMAIN     199    206       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   207    227       6 (POTENTIAL).
FT   DOMAIN     228    288       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   289    309       7 (POTENTIAL).
FT   DOMAIN     310    397       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   398    418       8 (POTENTIAL).
FT   DOMAIN     419    441       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   442    462       9 (POTENTIAL).
FT   DOMAIN     463    472       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   473    493       10 (POTENTIAL).
FT   DOMAIN     494    520       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   521    541       11 (POTENTIAL).
FT   DOMAIN     542    570       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   571    591       12 (POTENTIAL).
FT   DOMAIN     592    615       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD   353    353       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC   377    422       SASGPGLAFIVFTEAVLHMPGASVWSVLFFGMLFTLGLSSM
FT                               FGNME -> VLLCGLCSSLGCCLPWVCPPCLGTWRVSLHHY
FT                               WTWGSYPKVYPRRS (IN ISOFORM A8).
FT   VARSPLIC   377    444       SASGPGLAFIVFTEAVLHMPGASVWSVLFFGMLFTLGLSSM
FT                               FGNMEGVITPLLDMGILPKGIPKEVMT -> PTWKQISGAR
FT                               VLGEGCARLTSRVCEASVLP (IN ISOFORM B11 AND
FT                               ISOFORM B9).
FT   VARSPLIC   445    454       MISSING (IN ISOFORM A11).
FT   VARSPLIC   499    552       FCDDIEWMTGRRPGLYWQVTWRVVSPMLLFGIFLSYIVLLI
FT                               QTPPSYKAWNPQY -> NIFPQERRSSTQAGCRSPVCSCPS
FT                               CPHCGSLELLWLSYCPSTNRGGRLRIWKVV (IN
FT                               ISOFORM A10 AND ISOFORM B9).
FT   VARSPLIC   553    615       MISSING (IN ISOFORM A10).
SQ   SEQUENCE   615 AA;  69228 MW;  A7925C0397FC63F8 CRC64;


  Query Match           49.0%;  Score 47;  DB 11;  Length 615;
  Best Local Similarity  75.0%;  Pred. No. 8.5;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       5 SGHNSLFWYRQT 16
           ||  | ||||||
Db     154 SGTVSYFWYRQT 165


RESULT   3
Q62687
ID   Q62687      PRELIMINARY;      PRT;   615 AA.
AC   Q62687;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   RENAL OSMOTIC STRESS-INDUCED NA-CL ORGANIC SOLUTE COTRANSPORTER.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SPRAGUE-DAWLEY; TISSUE=KIDNEY CORTEX;
RX   MEDLINE=95029937; PubMed=7943364;
RA   Wasserman J.C., Delpire E., Tonidandel W., Kojima R., Gullans S.R.;
RT   "Molecular characterization of ROSIT, a renal osmotic stress-induced
RT   Na(+)-Cl(-)-organic solute cotransporter.";
RL   Am. J. Physiol. 267:F688-F694(1994).
DR   EMBL; U12973; AAC13771.1; -.
DR   InterPro; IPR000175; Na_neurotran_symport.
DR   Pfam; PF00209; SNF; 2.
DR   PRINTS; PR00176; NANEUSMPORT.
DR   PROSITE; PS50267; NA_NEUROTRAN_SYMP_3; 1.
SQ   SEQUENCE   615 AA;  69556 MW;  F41E7DE1DC276918 CRC64;


  Query Match           49.0%;  Score 47;  DB 11;  Length 615;
  Best Local Similarity  75.0%;  Pred. No. 8.5;
  Matches    9;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       5 SGHNSLFWYRQT 16
           ||  | ||||||
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Db    154 SGTVSYFWYRQT 165


RESULT   4
Q9FTF3
ID   Q9FTF3      PRELIMINARY;      PRT;   621 AA.
AC   Q9FTF3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   PUTATIVE RECEPTOR KINASE.
GN   P0463F06.16 OR OJ1212_B09.24.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NIPPONBARE;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT   clone:P0463F06.";
RL   Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NIPPONBARE;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT   clone:OJ1212_B09.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP002867; BAB17126.1; -.
DR   EMBL; AP003338; BAB39451.1; -.
DR   InterPro; IPR000719; Euk_pkinase.
DR   InterPro; IPR003015; HLH_Myc.
DR   InterPro; IPR002290; Ser_thr_kin_actsite.
DR   InterPro; IPR001245; Tyr_kin.
DR   Pfam; PF00069; pkinase; 1.
DR   SMART; SM00221; STYKc; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   ATP-binding; Kinase; Receptor; Transferase.
SQ   SEQUENCE   621 AA;  69776 MW;  8D241127786B99EF CRC64;


  Query Match             49.0%;  Score 47;  DB 10;  Length 621;
  Best Local Similarity   69.2%;  Pred. No. 8.6;
  Matches    9;  Conservative    1;  Mismatches    1;  Indels    2;  Gaps    1;

Qy      3 PIS--GHNSLFWY 13
          |||  |||: |||
Db    153 PISCLGHNNQFWY 165


RESULT   5
Q9SY90
ID   Q9SY90      PRELIMINARY;      PRT;   421 AA.
AC   Q9SY90;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   T25B24.5 PROTEIN.
GN   T25B24.5.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA   Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA   Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA   Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA   Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC005850; AAD25550.1; -.
SQ   SEQUENCE   421 AA;  48772 MW;  5B1ADF700118431E CRC64;


  Query Match             46.9%;  Score 45;  DB 10;  Length 421;
  Best Local Similarity   60.0%;  Pred. No. 13;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      6 GHNSLFWYRQ 15
          ||   :||||
Db    301 GHGGFYWYRQ 310


RESULT   6
Q9NN63
ID   Q9NN63      PRELIMINARY;      PRT;   981 AA.
AC   Q9NN63;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   POSSIBLE HYPOTHETICAL 46.8 KDA PROTEIN IN CLC1-PDS2 INTERGENIC REGION
DE   (FRAGMENT).
GN   LM15.368.
OS   Leishmania major.
OC   Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX   NCBI_TaxID=5664;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FRIEDLIN;
RA   Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL160371; CAC00347.1; -.
DR   InterPro; IPR000613; PseudoU_synth.
DR   InterPro; IPR002990; PSI_RLU.
DR   ProDom; PD001819; PseudoU_synth; 1.
DR   PROSITE; PS01129; PSI_RLU; 1.
FT   NON_TER       1       1
FT   NON_TER     981     981
SQ   SEQUENCE   981 AA;  103596 MW;  93B5C673F15204D2 CRC64;


  Query Match             46.4%;  Score 44.5;  DB 5;  Length 981;
  Best Local Similarity   53.3%;  Pred. No. 36;
  Matches    8;  Conservative    2;  Mismatches    2;  Indels    3;  Gaps    1;

Qy      1 CKPI---SGHNSLFW 12
          |:||     ||||:|
Db    696 CRPIGCLDHHNSLYW 710


RESULT   7
Q9D2W6
ID   Q9D2W6      PRELIMINARY;      PRT;   215 AA.
AC   Q9D2W6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   9130422I10RIK PROTEIN.
GN   9130422I10RIK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=CECUM;
RX   MEDLINE=21085660; PubMed=11217851;
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RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
DR   EMBL; AK018686; BAB31344.1; -.
DR   MGI; MGI:1918846; 9130422I10Rik.
SQ   SEQUENCE   215 AA;  23722 MW;  3C6B3C964E18ED3E CRC64;


  Query Match             45.8%;  Score 44;  DB 11;  Length 215;
  Best Local Similarity   41.7%;  Pred. No. 9.6;
  Matches    5;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 ISGHNSLFWYRQ 15
           ::|::|:||::|
Db     176 LAGYSSIFWWKQ 187


RESULT   8
Q99N04
ID   Q99N04      PRELIMINARY;      PRT;   234 AA.
AC   Q99N04;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MS4A7 PROTEIN.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MAMMARY GLAND;
RA   Liang Y., Tedder T.F.;
RT   "Identification of a CD20-, FcepsilonRIbeta-, and HTm4-Related Gene
RT   Family: Sixteen New MS4A Family Members Expressed in Human and
RT   Mouse.";
RL   Genomics 72:119-127(2001).
DR   EMBL; AF237917; AAK37607.1; -.
SQ   SEQUENCE   234 AA;  25754 MW;  CF88B968FBB0E33F CRC64;


  Query Match             45.8%;  Score 44;  DB 11;  Length 234;
  Best Local Similarity   41.7%;  Pred. No. 10;
  Matches    5;  Conservative    7;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       4 ISGHNSLFWYRQ 15
           ::|::|:||::|
Db     195 LAGYSSIFWWKQ 206


RESULT   9
Q9L2D5
ID   Q9L2D5      PRELIMINARY;      PRT;   428 AA.
AC   Q9L2D5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE   PUTATIVE SECRETED PROTEIN.
GN   SC7A8.23.
OS   Streptomyces coelicolor.
OC   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC   Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX   NCBI_TaxID=1902;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Oliver K., Harris D.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RA   Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=A3(2);
RX   MEDLINE=97000351; PubMed=8843436;
RA   Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J.,
RA   Kinashi H., Hopwood D.A.;
RT   "A set of ordered cosmids and a detailed genetic and physical map for
RT   the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
RL   Mol. Microbiol. 21:77-96(1996).
DR   EMBL; AL137187; CAB69772.1; -.
SQ   SEQUENCE   428 AA;  44436 MW;  11A30F3D74727C38 CRC64;


  Query Match             45.8%;  Score 44;  DB 2;  Length 428;
  Best Local Similarity   61.5%;  Pred. No. 19;
  Matches    8;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy       3 PISGHNSLFWYRQ 15
           | :| |  |||||
Db     108 PHAGLNGGFWYRQ 120


RESULT  10
Q9LPW2
ID   Q9LPW2      PRELIMINARY;      PRT;   556 AA.
AC   Q9LPW2;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   F13K23.13 PROTEIN.
GN   F13K23.13.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Liu S.X., Sakano H., Yu G., Lee J.M., Lenz C., Pham P., Toriumi M.,
RA   Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B., Liu A.,
RA   Vaysberg M., Altafi H., Brooks S., Buehler E., Chao Q., Conn L.,
RA   Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B.,
RA   Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W.,
RA   Ecker J.R., Federspiel N.A., Theologis A.;
RT   "The sequence of BAC F13K23 from Arabidopsis thaliana chromosome 1.";
RL   Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC012187; AAF78503.1; -.
DR   InterPro; IPR001810; F-box.
DR   Pfam; PF00646; F-box; 1.
DR   SMART; SM00256; FBOX; 1.
DR   PROSITE; PS50181; FBOX; 1.
SQ   SEQUENCE   556 AA;  65033 MW;  1D6DB8C95214BF10 CRC64;


  Query Match             45.8%;  Score 44;  DB 10;  Length 556;
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  Best Local Similarity   40.0%;  Pred. No. 25;
  Matches    6;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy      2 KPISGHNSLFWYRQT 16
          || | : :|:|: :|
Db    239 KPASANGTLYWFTET 253


RESULT  11
Q90770
ID   Q90770      PRELIMINARY;      PRT;   235 AA.
AC   Q90770;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   CD8 ALPHA CHAIN PRECURSOR.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RPL LINE 7 (INBRED); TISSUE=SPLEEN;
RX   MEDLINE=95238946; PubMed=7722305;
RA   Tregaskes C.A., Kong F.K., Paramithiotis E., Chen C.L.H.,
RA   Ratcliffe M.J.H., Davison T.F., Young J.R.;
RT   "Identification and analysis of the expression of CD8 alpha beta and
RT   CD8 alpha alpha isoforms in chickens reveals a major TCR-gamma delta
RT   CD8 alpha beta subset of intestinal intraepithelial lymphocytes.";
RL   J. Immunol. 154:4485-4494(1995).
CC   -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC       DOMAIN.
DR   EMBL; Z22726; CAA80421.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
KW   Signal.
FT   SIGNAL       1     19       POTENTIAL.
FT   CHAIN       20    235       CD8 ALPHA CHAIN.
SQ   SEQUENCE   235 AA;  26100 MW;  525326EE1AA4B512 CRC64;


  Query Match             44.8%;  Score 43;  DB 13;  Length 235;
  Best Local Similarity   40.0%;  Pred. No. 15;
  Matches    6;  Conservative    3;  Mismatches    6;  Indels    0;  Gaps    0;

Qy      1 CKPISGHNSLFWYRQ 15
          |:| :  | : | ||
Db     49 CRPFNSDNGVSWIRQ 63


RESULT  12
Q98337
ID   Q98337         PRELIMINARY;   PRT;   331 AA.
AC   Q98337;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
DE   SPIKE PROTEIN (FRAGMENT).
OS   murine hepatitis virus.
OC   Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC   Coronaviridae; Coronavirus.
OX   NCBI_TaxID=11138;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MHV-1;
RX   MEDLINE=96183918; PubMed=8642698;
RA   Suzuki H., Taguchi F.;
RT   "Analysis of the receptor-binding site of murine coronavirus spike
RT   protein.";
RL   J. Virol. 70:2632-2636(1996).
DR   EMBL; D83333; BAA11889.1; -.
FT   NON_TER     331    331
SQ   SEQUENCE   331 AA;  36854 MW;  F0CECA89DF352802 CRC64;


  Query Match             44.8%;  Score 43;  DB 12;  Length 331;
  Best Local Similarity   53.3%;  Pred. No. 22;
  Matches    8;  Conservative    3;  Mismatches    2;  Indels    2;  Gaps    1;

Qy      1 CKPISGHNSL--FWY 13
          ||| :| ||:  ||:
Db    166 CKPNTGGNSIIGFWH 180


RESULT  13
P94013
ID   P94013      PRELIMINARY;      PRT;   381 AA.
AC   P94013;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   W-3 FATTY ACID DESATURASE.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IR36, AND NIPPONBARE;
RA   Akagi H.;
RL   Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; D78506; BAA11397.1; -.
DR   EMBL; D78505; BAA11396.1; -.
DR   Mendel; 9612; Orysa;1208;9612.
DR   InterPro; IPR001225; FA_desaturase.
DR   Pfam; PF00487; FA_desaturase; 1.
DR   ProDom; PD001081; FA_desaturase; 1.
SQ   SEQUENCE   381 AA;  43640 MW;  4ED35EDCFE61C72D CRC64;


  Query Match             44.8%;  Score 43;  DB 10;  Length 381;
  Best Local Similarity   77.8%;  Pred. No. 25;
  Matches    7;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      6 GHNSLFWYR 14
          ||| | |||
Db    259 GHNDLPWYR 267


RESULT  14
Q9GF60
ID   Q9GF60      PRELIMINARY;      PRT;   504 AA.
AC   Q9GF60;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MATURASE K.
GN   MATK.
OS   Arabis lyallii.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabis.
OX   NCBI_TaxID=81977;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Koch M., Mitchell-Olds T.;
RT   "Evolutionary analysis of plastidic maturase K and nuclear chalcone
RT   synthase and their utility for phylogenetic reconstructions within the
RT   Brassicaceae.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF144332; AAG43301.1; -.
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DR   InterPro; IPR000442; Intron_maturse2.
DR   InterPro; IPR002866; MatK_N.
DR   Pfam; PF01348; Intron_maturas2; 1.
DR   Pfam; PF01824; MatK_N; 1.
KW   Chloroplast.
SQ   SEQUENCE   504 AA;  60319 MW;  94B8D6241DDAA6E4 CRC64;


  Query Match           44.8%;  Score 43;  DB 8;  Length 504;
  Best Local Similarity  58.3%;  Pred. No. 33;
  Matches    7;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 PISGHNSLFWYR 14
           |  || |||:|:
Db      86 PFLGHTSLFYYQ 97


RESULT  15
Q9GF49
ID   Q9GF49      PRELIMINARY;      PRT;   504 AA.
AC   Q9GF49;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE   MATURASE K.
GN   MATK.
OS   Arabis drummondii.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabis.
OX   NCBI_TaxID=72658;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ADRUM1;
RA   Koch M., Mitchell-Olds T.;
RT   "Evolutionary analysis of plastidic maturase K and nuclear chalcone
RT   synthase and their utility for phylogenetic reconstructions within the
RT   Brassicaceae.";
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF144343; AAG43312.1; -.
DR   InterPro; IPR000442; Intron_maturse2.
DR   InterPro; IPR002866; MatK_N.
DR   Pfam; PF01348; Intron_maturas2; 1.
DR   Pfam; PF01824; MatK_N; 1.
KW   Chloroplast.
SQ   SEQUENCE   504 AA;  60309 MW;  54062005ADF12C19 CRC64;


  Query Match           44.8%;  Score 43;  DB 8;  Length 504;
  Best Local Similarity  58.3%;  Pred. No. 33;
  Matches    7;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy       3 PISGHNSLFWYR 14
           |  || |||:|:
Db      86 PFLGHTSLFYYQ 97


Search completed: February  9, 2002, 10:53:55
Job time: 198 sec
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